92780

STIC-Biotech/ChemLib

From: Ibrahim, Medina A.
Sent: Tuesday, April 29, 2003 6:15 PM
To: STIC-Biotech/ChemLib
Subject: 10/010, 731

Please run the following search:

1. A nucleotide sequence from position 18 to 507 of SEQ ID NO:10
2. A nucleotide sequence from position 105 to 242 of SEQ ID NO:13. Thanks

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9203

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Date Completed: 5/8/03
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 03:16:57 ; Search time 273.089 Seconds
(without alignments)
4040.728 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507
Perfect score: 490
Sequence: 1 TGTCAAACACACACATAACA.....CAAAAAAAAAAAAAAAAAA 490

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488	99.6	507	19	AAV39195	Antifungal polypep
2	486.4	99.3	490	19	AAV39186	Antifungal polypep
3	301.8	61.6	327	19	AAV39194	Antifungal polypep
4	234	47.8	250	19	AAV39187	Alfalfa plant anti
5	228.6	46.7	293	19	AAV39191	Antifungal polypep
6	208	42.4	468	21	AAZ49412	Pea Defensin prote
7	179.8	36.7	200	19	AAV39190	Antifungal polypep
8	127.4	26.0	494	22	AAD17530	Soybean Gly m2 pro
9	54	11.0	62	19	AAV39196	Antifungal polypep
c 10	49.4	10.1	16633	24	ABN79985	Human chemically m
c 11	48.6	9.9	9963	24	ABL32694	Human immune syste
c 12	46	9.4	6169	22	AAS46370	Tumour suppressor
c 13	46	9.4	6169	24	ABN80097	Human chemically m
c 14	46	9.4	6557	24	ABL33001	Human immune syste
15	46	9.4	11922	21	AAA70187	Plasmodium falcipa
c 16	45.8	9.3	6012	24	ABL34058	Human immune syste
c 17	45.4	9.3	83391	24	ABQ67094	Human angiogenesis
c 18	45.2	9.2	5997	24	ABL33625	Human immune syste
c 19	45.2	9.2	6392	24	ABL32684	Human immune syste
c 20	45.2	9.2	6392	24	ABL34506	Human metastasis a
c 21	45	9.2	7025	24	ABK40060	Human chemically p
c 22	45	9.2	7025	24	AAS63351	Chemically pretrea
c 23	45	9.2	11029	22	AAS46414	Tumour suppressor
c 24	44.8	9.1	1216	24	ABL34361	Human immune syste
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c 26	44.6	9.1	8182	24	ABN80221	Human chemically m
c 27	44.6	9.1	9155	24	ABL32463	Human immune syste
c 28	44.6	9.1	13584	24	ABL32615	Human immune syste
c 29	44.4	9.1	6533	24	ABL33709	Human immune syste
c 30	44.4	9.1	16217	24	ABL32624	Human immune syste
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c 33	44.4	9.1	640681	24	ABA92787	Buchnera sp. genom
c 34	44.2	9.0	9515	22	AAS45453	Chemically pretrea
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c 36	44.2	9.0	9515	24	ABK28308	DNA transcription
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c 39	44	9.0	7110	24	ABL33557	Human immune syste
c 40	44	9.0	7110	24	AAS61291	Human gene regulat
c 41	44	9.0	34688	24	ABQ67060	Human angiogenesis
c 42	43.6	8.9	7498	24	ABL32257	Human immune syste
c 43	43.6	8.9	18154	24	ABL32254	Human immune syste
c 44	43.4	8.9	6222	24	ABL32239	Human immune syste
c 45	43.4	8.9	6228	24	ABL70470	Chemically treated

ALIGNMENTS

RESULT 1
AAV39195
ID AAV39195 standard; DNA; 507 BP.
XX
AC AAV39195;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfAFP1 mature sequence encoding DNA.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 173..310
FT /*tag= a
FT /product= "mature AlfALFP1"
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX

```
DR   WPI; 1998-348537/30.
DR   P-PSDB; AAW61964.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 5; Page 77; 97pp; English.
XX
CC   This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC   alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2  are
CC   useful to control plant fungi, especially pathogenic fungi, by
CC   transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other;

  Query Match             99.6%;  Score 488;  DB 19;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-107;
  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360
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Qy     481 AAAAAAAAA 490
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RESULT 2
AAV39186
ID   AAV39186 standard; DNA; 490 BP.
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AC   AAV39186;
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DT   01-OCT-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP1 encoding cDNA.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ss.
XX
OS   Medicago sativa.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     75..155
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XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
DR   P-PSDB; AAW61967.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 5; Fig 1; 97pp; English.
XX
CC   This cDNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC   alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2  are
CC   useful to control plant fungi, especially pathogenic fungi, by
CC   transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other;

  Query Match             99.3%;  Score 486.4;  DB 19;  Length 490;
  Best Local Similarity   99.8%;  Pred. No. 6.2e-107;
  Matches  489;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy    421 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 480
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Db    481 AAAAAAAAA 490
```

RESULT 3
AAV39194
ID AAV39194 standard; DNA; 327 BP.
XX
AC AAV39194;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfAFP2 3' region.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS Medicago sativa.
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX
DR WPI; 1998-348537/30.
XX
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 77; 97pp; English.
XX
CC This sequence represents the 3' region of the DNA encoding an antifungal
CC polypeptide, AlfAFP2 isolated from alfalfa plants (Medicago). The
CC polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
CC especially pathogenic fungi, by transforming plant cells with a vector
CC comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
CC antifungally effective amounts of the polypeptide. Such transformed
CC plants may be e.g. apple, wheat, cotton and especially potato.
CC Micro-organisms may also be transformed to produce the polypeptides, and
CC applied to plants to control plant fungi. The polypeptides can also be
CC included with a suitable solvent in antifungal compositions and these can
CC be administered to plants to control plant fungi. Such compositions and
CC genetically engineered plants may also contain additional molecules e.g.
CC the compositions can contain other antifungal agents or the plants
CC contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC proteins. The polypeptides are also useful to prepare antibodies useful
CC to detect polypeptides or isolate other alfalfa plant antifungal protein
CC antigens. The nucleic acids are useful to produce polypeptides and
CC transgenic plants and as probes or primers in nucleic acid hybridisation
CC e.g. to detect complementary sequences in samples, and to prepare mutants
CC or isolate similar sequences from related species.
XX
SQ Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other;

Query Match 61.6%; Score 301.8; DB 19; Length 327;
Best Local Similarity 97.6%; Pred. No. 7.2e-63;
Matches 319; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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Qy    285 AGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAA 344
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Qy    404 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 463
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Qy    464 TCGTNTCCAAAAAAAAAAAAAAAAAAA 490
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Db    301 TCGTNTCCAAAAAAAAAAAAAAAAAAA 327
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RESULT 4
AAV39187
ID AAV39187 standard; DNA; 250 BP.
XX
AC AAV39187;
XX
DT 25-SEP-1998 (first entry)
XX
DE Alfalfa plant antifungal polypeptide AlfALFP1 encoding DNA.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 105..242
FT /*tag= a
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XX
PN WO9826083-A1.
XX

PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX
DR WPI; 1998-348537/30.
DR P-PSDB; AAW61964.
XX
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 3; Page 78; 97pp; English.
XX
CC This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2 are
CC useful to control plant fungi, especially pathogenic fungi, by
CC transforming plant cells with a vector comprising sequences encoding
CC AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other;

Query Match 47.8%; Score 234; DB 19; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 68

Qy     120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 128

Qy     180 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 188

Qy     240 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 293
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 242
```

RESULT 5
AAV39191
ID AAV39191 standard; DNA; 293 BP.
XX
AC AAV39191;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfAFP2 coding sequence.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS Medicago sativa.
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX
DR WPI; 1998-348537/30.
XX
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Claim 18; Page 75; 97pp; English.
XX
CC This represents a coding sequence of an antifungal polypeptide, AlfAFP2
CC isolated from alfalfa plants (Medicago). The polypeptides AlfAFP1 and
CC AlfAFP2 are useful to control plant fungi, especially pathogenic fungi,
CC by transforming plant cells with a vector comprising sequences encoding
CC AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC cotton and especially potato. Micro-organisms may also be transformed
CC to produce the polypeptides, and applied to plants to control plant
CC fungi. The polypeptides can also be included with a suitable solvent in
CC antifungal compositions and these can be administered to plants to
CC control plant fungi. Such compositions and genetically engineered plants
CC may also contain additional molecules e.g. the compositions can contain
CC other antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;

Query Match 46.7%; Score 228.6; DB 19; Length 293;
Best Local Similarity 89.1%; Pred. No. 2.2e-45;
Matches 246; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

```
Qy       1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy      61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db      78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCCTCGTTC 137

Qy     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
           ||||||||| |||||||||| ||||||| || ||    || ||||||||||||||  | |
Db     138 TCTTTGTTGAACAAGAAATTATGGTGACCGAGGCAGCTACTTGTGAGAATTTGGCTAACA 197

Qy     181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
           ||| ||||||||||||||  ||||||||||  ||||||| |||||||| ||  | |
Db     198 CATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCACTGCAAAACCAAAGAACACTTAC 257

Qy     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
           |||| || ||||| |||||||||||||||||||| |
Db     258 TTAGCGGNAGGTGCAGGGACGACTTCCGCTGCTGCT 293
```

```
RESULT 6
AAZ49412
ID   AAZ49412 standard; cDNA; 468 BP.
XX
AC   AAZ49412;
XX
DT   04-APR-2000  (first entry)
XX
DE   Pea Defensin protein Drr230, encoding cDNA.
XX
KW   Transgenic plant; disease resistance; DRR206; defensin; Drr230; PR10.1;
KW   chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;
KW   CaMV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;
KW   Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.
XX
OS   Pisum sativum.
XX
FH   Key             Location/Qualifiers
FT   CDS             78..296
FT                   /*tag= a
FT                   /product= "Pea Defensin protein, Drr230"
FT                   /note= "Confers resistance against fungal and bacterial
FT                   pathogens"
XX
PN   WO200001824-A2.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-CA00608.
XX
PR   03-JUL-1998;   98CA-2242116.
PR   06-JUL-1998;   98US-0091751.
XX
PA   (UYMA-) UNIV MANITOBA.
XX
PI   Fristensky B,  Wang Y;
XX
DR   WPI; 2000-126938/11.
DR   P-PSDB; AAY44509.
XX
PT   Recombinant expression system for expressing DRR206 or defensin, used
PT   to produce pathogen resistant Brassica napus  -
XX
PS   Claim 11; Fig 9; 39pp; English.
XX
CC   The present sequence is the cDNA encoding defensin protein, derived from
CC   the clone Drr230 of Pea. This sequence is strongly induced by bacterial
CC   and fungal pathogens like, blackleg fungus. This gene is used in a
CC   recombinant expression system, capable of transforming plants like,
CC   Canola (Brassica napus), under the constitutive control of CaMV 35S
CC   inducible promoter, responsive to pathogen infections. T-DNA sequence is
CC   also present, for integration of the expression system into the plant
CC   genome. Transgenic plants expressing DRR206 and defensin protein,
CC   inhibited fungal growth in-vitro and are resistant to pathogenic
CC   infections of Rhizoctonia solani, Leptosphaeria maculans and Sclerotinia
CC   sclerotiorum.
XX
SQ   Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;

  Query Match             42.4%;  Score 208;  DB 21;  Length 468;
  Best Local Similarity   72.2%;  Pred. No. 2e-40;
  Matches  345;  Conservative    0;  Mismatches  112;  Indels   21;  Gaps    5;

Qy       4 CAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAAT 63
           || | |||||||||||||| |      |||||||||   |  | | ||||||||||| |
Db       6 CACAAACACACATAACACATTAAGTGAAGTGAGTCATATTAAGTTTTTATATTCATCACT 65

Qy      64 -CTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTC 122
            || |  || | ||||||||||||||||||||||| |||| | ||||||| || | ||||||
Db      66 ACTTAAGAAGCCATGGAGAAGAAATCACTAGCTTGCTTGTCCTTCCTCCTCCTCGTTCTC 125

Qy     123 TTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAA 182
           |||||||||||||||| |||||||  ||||| |  |||||||||||||||||| | |  |

Db     126 TTTGTTGCACAAGAAATAGTGGTGAGTGAAGCAAACACATGTGAGAATTTGGCTGGTTCA 185

Qy     183 TATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTT 242
           |||| ||||  |||||| |||| |||||| |||||| | |||  |||||  |||| ||
Db     186 TATAAGGGAGTATGCTTCGGTGGATGTGACCGTCACTGTAGAACACAAGAGGGCGCAATT 245

Qy     243 AGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTC 302
           || || || || ||||| ||||| ||||| ||||| ||||||| |||||||| | |
Db     246 AGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGCACTAAAAACTGTTAAATCCCTTTT 305

Qy     303 CTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCA 362
           |||||||| ||| |    |     ||| |   ||||||| || |||||||| |
Db     306 CTCCAACACCAACAACACCCATATATAAT-ACTATAATATAAATAAATAAACA------- 357

Qy     363 CGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGT 422
                 |  | |    |    ||||| | | | |||||||||||| | |||||||| || ||
Db     358 ------AGTGTTGTTTCGAATTCTATGTGTGT-ACTCAATATCGTGTATAACGTGTTTGT 410

Qy     423 TATGCACTT-----CTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAA 475
           |||||||||      |||||||||||||||| |  ||| | | ||||| | |||||||
Db     411 TATGCACTTTTATCATATCATATGGAATAAAAAGTAATCAATCATTTCCTTTCCAAAA 468


RESULT 7
AAV39190
ID   AAV39190 standard; DNA; 200 BP.
XX
AC   AAV39190;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP2 5' region.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS   Medicago sativa.
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 18; Page 75; 97pp; English.
XX
CC   This sequence represents the 5' region of the DNA encoding an antifungal
CC   polypeptide, AlfAFP2 isolated from alfalfa plants (Medicago). The
CC   polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
CC   especially pathogenic fungi, by transforming plant cells with a vector
CC   comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
CC   antifungally effective amounts of the polypeptide. Such transformed
CC   plants may be e.g. apple, wheat, cotton and especially potato.
CC   Micro-organisms may also be transformed to produce the polypeptides, and
CC   applied to plants to control plant fungi. The polypeptides can also be
CC   included with a suitable solvent in antifungal compositions and these can
CC   be administered to plants to control plant fungi. Such compositions and
CC   genetically engineered plants may also contain additional molecules e.g.
CC   the compositions can contain other antifungal agents or the plants
CC   contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC   proteins. The polypeptides are also useful to prepare antibodies useful
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CC   to detect polypeptides or isolate other alfalfa plant antifungal protein
CC   antigens. The nucleic acids are useful to produce polypeptides and
CC   transgenic plants and as probes or primers in nucleic acid hybridisation
CC   e.g. to detect complementary sequences in samples, and to prepare mutants
CC   or isolate similar sequences from related species.
XX
SQ   Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other;

  Query Match             36.7%;  Score 179.8;  DB 19;  Length 200;
  Best Local Similarity   98.9%;  Pred. No. 9.2e-34;
  Matches  181;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      94 CTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 153
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 CAGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 77

Qy     154 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 137

Qy     214 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 197

Qy     274 GGT 276
           | |
Db     198 GCT 200


RESULT 8
AAD17530
ID   AAD17530 standard; cDNA; 494 BP.
XX
AC   AAD17530;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Soybean Gly m2 protein encoding cDNA from clone sls1c.pk027.a11.
XX
KW   Soybean; allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1;
KW   soybean vacuolar protein; Gly m IA; Gly m IB; rGLY m3; Glycinin G1;
KW   alaB1b; food; infant formula; animal feed; coating; salad oil; syrup;
KW   spraying oil; roasting oil; frying oil; cracker; confectionery product;
KW   snack food; topping; sauce; batter; breading mixture; baking mix; dough;
KW   Gly m2 protein; clone sls1c.pk027.a11; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..273
FT                   /*tag= a
FT                   /product= "Soybean Gly m2 protein"
XX
PN   WO200168887-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-US08254.
XX
PR   16-MAR-2000; 2000US-0189823.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Jung R,  Kinney AJ;
XX
DR   WPI; 2001-582460/65.
DR   P-PSDB; AAE10361.
XX
PT   Recombinant expression construct to lower allergen (e.g. Gly m Bd 30K)
PT   content of a soybean, comprises a nucleic acid fragment encoding the
PT   allergen, useful for producing soybean plants which can be used to make
PT   soybean products -
XX
PS   Example 7; Page 51-52; 57pp; English.
XX
CC   The patent discloses hypoallergenic transgenic soybeans and recombinant
CC   expression constructs to lower soybean vacuolar protein, commonly known
CC   as P34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA,
CC   Gly m IB, rGLY m3 or Glycinin G1 (alaB1b). The allergen content of the
CC   soybean is reduced by sense suppression which is accomplished by using
CC   the expression construct that comprises a nucleic acid fragment encoding
CC   the allergen. The constructs are useful for producing hypoallergenic
CC   transgenic soybean plants which can be used to make hypoallergenic
CC   soybean products which can be used in a variety of food (e.g. infant
CC   formulas) and animal feed applications. The oil made from seeds of the
CC   hypoallergenic transgenic soybean plants can be used as ingredients,
CC   as coatings, as salad oils, as spraying oils, as roasting oils, and
CC   as frying oils. The foods in which the oil may be used include crackers
CC   and snack foods, confectionery products, syrups and toppings, sauces,
CC   batter and breading mixtures, baking mixes and doughs. The present
CC   sequence is soybean Gly m2 protein encoding cDNA from sls1c.pk027.a11
CC   clone. This sequence is a minor soybean seed allergen.
XX
SQ   Sequence 494 BP; 153 A; 97 C; 103 G; 134 T; 7 other;

  Query Match             26.0%;  Score 127.4;  DB 22;  Length 494;
  Best Local Similarity   68.4%;  Pred. No. 3.6e-21;
  Matches  225;  Conservative    0;  Mismatches   91;  Indels   13;  Gaps    3;

Qy      46 TTATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCT 105
           ||| ||| |          ||||| || | ||||||||||||||| ||||||| || ||||
Db      17 TTACATACACGTGAATCACTAATTAAGCCATGGAGAAGAAATCAATAGCTGGGTTGTGCT 76

Qy     106 TCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACAT 162
           |||||||| | |||||||||||||| |||||| |||||||    || || || |  || |
Db      77 TCCTCTTCCTTGTTCTCTTTGTTGCTCAAGAAGTTGTGGTGCAAACTGAGGCAAAGACTT 136

Qy     163 GTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTC 216
           | |||||  |||| |||| ||| ||||| ||||||||      | |  | || ||   ||
Db     137 GCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGATGATC 196

Qy     217 ACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
           ||||||  | ||||||| ||    | || || || || |||||||| || ||||| ||||
Db     197 ACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGTTGGT 256

Qy     277 GTACTAAAAGATGTTAAATGGATC----TCCTCCAACATCAAGATGTGCATGGAATAGTC 332
           | || ||||  |||||||||||||      ||||||| | |||| |      | |  |
Db     257 GCACCAAAAACTGTTAAATGGATCCATTCACTCCAACGTGAAGAAGATGCATGCAGCGCT 316

Qy     333 TTTATAATAAAACTAAATAAATAAAATGC 361
           || ||  |||| || |   |  | || |
Db     317 ATTTTATAAAAAATACAACTACTATATAC 345


RESULT 9
AAV39196
ID   AAV39196 standard; DNA; 62 BP.
XX
AC   AAV39196;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP2 5' gene specific primer.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.
XX
OS   Synthetic.
OS   Medicago sativa.
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
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XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Example 4; Page 78; 97pp; English.
XX
CC   This primer is used for the PCR amplification of the cDNA encoding an
CC   antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and
CC   AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control
CC   plant fungi, especially pathogenic fung, by transforming plant cells
CC   with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow
CC   expression of antifungally effective amounts of the polypeptide. Such
CC   transformed plants may be e.g. apple, wheat, cotton and especially
CC   potato. Micro-organisms may also be transformed to produce the
CC   polypeptides, and applied to plants to control plant fungi. The
CC   polypeptides can also be included with a suitable solvent in antifungal
CC   compositions and these can be administered to plants to control plant
CC   fungi. Such compositions and genetically engineered plants may also
CC   contain additional molecules e.g. the compositions can contain other
CC   antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 62 BP; 18 A; 15 C; 12 G; 17 T; 0 other;

  Query Match             11.0%;  Score 54;  DB 19;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 0.00082;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTC 113
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTC 62


RESULT 10
ABN79985/c
ID   ABN79985 standard; DNA; 16633 BP.
XX
AC   ABN79985;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human chemically modified disease associated gene SEQ ID NO 2.
XX
KW   Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KW   heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KW   dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KW   antidiabetic; cytostatic; anticonvulsant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200200927-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07536.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130908/17.
XX
PT   Novel nucleic acid useful for diagnosis and therapy of diseases
PT   associated with development genes such as diabetes, comprises a
PT   sequence of a segment of chemically pretreated DNA of genes associated
PT   with development  -
XX
PS   Claim 1; SEQ ID NO 2; 27pp; English.
XX
CC   The invention relates to a nucleic acid (I) comprising a sequence at
CC   least 18 bases in length of a segment of chemically pretreated DNA (II)
CC   of genes associated with development selected from 87 genes listed in
CC   the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350
CC   sequences (ABN79984-ABN80333) or their complements. The invention is
CC   useful for the diagnosis or therapy of diseases associated with
CC   development genes, in particular disease related to homeobox containing
CC   genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
CC   associated with congenital heart disease, epilepsy, diseases related to
CC   histone deacetylation, Currarino syndrome, diseases related with the
CC   development of the brain and limb girdle muscular dystrophy and dwarfism.
CC   Oligomers specific to each of the genes are useful for detecting the
CC   methylation state of all CpG dinucleotides within the 350 sequences or
CC   (II) and their complementary sequences, as primer oligonucleotides for
CC   the amplification of the 350 sequences, (II) and/or their complements and
CC   as oligomer probes for detecting the cytosine methylation state and/or
CC   single nucleotide polymorphisms (SNPs).
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification but is based on sequence information supplied to Derwent by
CC   the European Patent Office.
XX
SQ   Sequence 16633 BP; 5259 A; 142 C; 3255 G; 7977 T; 0 other;

  Query Match             10.1%;  Score 49.4;  DB 24;  Length 16633;
  Best Local Similarity   52.2%;  Pred. No. 0.032;
  Matches  107;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy     284 AAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAA 343
           || || |||  |  ||||  | |||| | || ||   ||     || |||||| ||   |
Db   14559 AAAATCTTATTTATATCTTTTTCAACTTTAATATCCCCACTTTTTAATCTTTAAAAATTA 14500

Qy     344 ACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATA 403
           |  |   ||   |||   |   |  ||| | | ||| | |  || | ||||   |  ||
Db   14499 AAAACCAAATATAAACAAAAAAAAAATAACCAAAACATTAAATAAACATATATATACATT 14440

Qy     404 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 463
           ||     |       ||  ||. | || ||  | ||    ||||||  ||     || |
Db   14439 TCATAATTTTTACCATACCTAATAAATTATACTAAATTTCTTAAACAAAAAACCTAAAAT 14380

Qy     464 TCGTNTCCAAAAAAAAAAAAAAAAA 488
           ||   | | |  ||||||| |||||
Db   14379 TCTATTACCACCAAAAAAACAAAAA 14355


RESULT 11
ABL32694/c
ID   ABL32694 standard; DNA; 9963 BP.
XX
AC   ABL32694;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 667.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
```

KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 667; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 9963 BP; 2520 A; 180 C; 2578 G; 4685 T; 0 other;

Query Match 9.9%; Score 48.6; DB 24; Length 9963;
Best Local Similarity 51.7%; Pred. No. 0.045;
Matches 108; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 282 AAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATA 341
Db 3726 ACAAATTACTTAAACTTTCTCTACCTCAACTTCCTTCTCTATATAATATTAATAATAATA 3667

Qy 342 AAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAA 401
Db 3666 ATTCCTACTTCACAAAATTAATATAAAAATAAAATAAATTAATATTTATAAAACACCTAA 3607

Qy 402 TATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAA 461
Db 3606 AATAATACCTAACATATACAAATTATATATATATAAAAAAAAAAAAAAAAAAAAAAAAAA 3547

Qy 462 TTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
Db 3546 AAAAAAAAAAAAAAAAAAAAATAAAAAAA 3518

RESULT 12
AAS46370/c
ID AAS46370 standard; DNA; 6169 BP.
XX
AC AAS46370;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #92.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP02955.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer -
XX
PS Claim 1; SEQ ID No 92; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 6169 BP; 1840 A; 112 C; 1192 G; 3025 T; 0 other;

Query Match 9.4%; Score 46; DB 22; Length 6169;
Best Local Similarity 56.9%; Pred. No. 0.17;
Matches 82; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 347 AAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCG 406
Db 2534 AAATAAATCTTACAATTAATATATAAATTTAACTTAATACTTCTTTTTTCTTTTTTATTC 2475

Qy 407 NGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCG 466
Db 2474 TACAAAAACTATTCTTAAATAACTTATATATTTTACAATAAATAACACTAAATAATCTCA 2415

Qy 467 TNTCCAAAAAAAAAAAAAAAAAAA 490
Db 2414 AAAAAAAAATAAAAATAAATAAAA 2391

```
RESULT 13
ABN80097/c
ID   ABN80097 standard; DNA; 6169 BP.
XX
AC   ABN80097;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human chemically modified disease associated gene SEQ ID NO 114.
XX
KW   Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KW   heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KW   dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KW   antidiabetic; cytostatic; anticonvulsant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200200927-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07536.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130908/17.
XX
PT   Novel nucleic acid useful for diagnosis and therapy of diseases
PT   associated with development genes such as diabetes, comprises a
PT   sequence of a segment of chemically pretreated DNA of genes associated
PT   with development  -
XX
PS   Claim 1; SEQ ID NO 114; 27pp; English.
XX
CC   The invention relates to a nucleic acid (I) comprising a sequence at
CC   least 18 bases in length of a segment of chemically pretreated DNA (II)
CC   of genes associated with development selected from 87 genes listed in
CC   the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350
CC   sequences (ABN79984-ABN80333) or their complements. The invention is
CC   useful for the diagnosis or therapy of diseases associated with
CC   development genes, in particular disease related to homeobox containing
CC   genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
CC   associated with congenital heart disease, epilepsy, diseases related to
CC   histone deacetylation, Currarino syndrome, diseases related with the
CC   development of the brain and limb girdle muscular dystrophy and dwarfism.
CC   Oligomers specific to each of the genes are useful for detecting the
CC   methylation state of all CpG dinucleotides within the 350 sequences or
CC   (II) and their complementary sequences, as primer oligonucleotides for
CC   the amplification of the 350 sequences, (II) and/or their complements and
CC   as oligomer probes for detecting the cytosine methylation state and/or
CC   single nucleotide polymorphisms (SNPs).
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification but is based on sequence information supplied to Derwent by
CC   the European Patent Office.
XX
SQ   Sequence 6169 BP; 1840 A; 112 C; 1192 G; 3025 T; 0 other;

  Query Match             9.4%;  Score 46;  DB 24;  Length 6169;
  Best Local Similarity   56.9%;  Pred. No. 0.17;
  Matches   82;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy     347 AAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCG 406
           ||||||||   |         ||||  |  ||||| ||   | | | |   |   |||
Db    2534 AAATAAATCTTACAATTAATATATAAATTTAACTTAATACTTCTTTTTTCTTTTTTATTC 2475

Qy     407 NGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCG 466
           || ||  ||||  | |   |||| ||| | |  |||||| | || ||| |||| ||
Db    2474 TACAAAAACTATTCTTAAATAACTTATATATTTTACAATAAATAACACTAAATAATCTCA 2415

Qy     467 TNTCCAAAAAAAAAAAAAAAAAAA 490
               |||| ||||| ||| ||||
Db    2414 AAAAAAAAATAAAAATAAATAAAA 2391


RESULT 14
ABL33001/c
ID   ABL33001 standard; DNA; 6557 BP.
XX
AC   ABL33001;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 974.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 974; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 6557 BP; 1748 A; 211 C; 1536 G; 3061 T; 1 other;

  Query Match             9.4%;  Score 46;  DB 24;  Length 6557;
  Best Local Similarity   52.1%;  Pred. No. 0.17;
  Matches  100;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy     298 ATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAA 357
           ||||||  | |    | ||        ||  || | | |   | || || |  ||| |||||||
Db    4437 ATCTCCACTACTCTTAACTAAAAAATCAAAAACTTTAAAAAAAAAATAAAAAAAAAATAAA 4378

Qy     358 ATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTA 417
           ||   | || |   | |||| ||| | ||| || | ||||||  |   | |||| |
Db    4377 TCCCAAAAAATAAATAAATAACTACATAAAAATAAATAAATCAATACCACTCTTAACCTC 4318
```

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Qy    418 TTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAA 477
          ||| | |     |   | | | |       |  ||  ||         |     |||||
Db   4317 TTAATAAACTCATCACAACCTTTCATTCCCAACTCCTAAACATTACAATTAAAACAAAAA 4258

Qy    478 AAAAAAAAAAAA 489
          ||||| ||||||
Db   4257 AAAAATAAAAAA 4246
```

RESULT 15
AAA70187
ID AAA70187 standard; DNA; 11922 BP.
XX
AC AAA70187;
XX
DT 07-NOV-2000 (first entry)
XX
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:320.
XX
KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;
KW antimalarial; malaria; protozoacide; infection; insecticide; ds.
XX
OS Plasmodium falciparum.
XX
PN WO200025728-A2.
XX
PD 11-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US26796.
XX
PR 05-NOV-1998; 98US-0107131.
XX
PA (HOFF/) HOFFMAN S.
PA (CARU/) CARUCCI D.
PA (GARD/) GARDNER M.
PA (VENT/) VENTER J C.
XX
PI Hoffman S, Carucci D, Gardner M, Venter JC;
XX
DR WPI; 2000-365347/31.
XX
PT Proteins encoded by chromosome 2 of the human malarial parasite,
PT Plasmodium falciparum, useful as antimalarial vaccines and in the
PT diagnosis of P.falciparum infection -
XX
PS Disclosure; Page 516-519; 577pp; English.
XX
CC The present invention describes proteins and their fragments (I) encoded
CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum.
CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2)
CC vaccines against P. falciparum infection comprising (I) or (II).
CC (I) and (II) are useful for the development of vaccines against
CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal
CC antibody raised to immunogens comprising the sequences of (I), are
CC useful in the detection of infection with P. falciparum. Furthermore,
CC (I) (especially when they are rifins or secreted or membrane proteins)
CC can aid the identification of drugs to treat or prevent P. falciparum
CC infection, or they can be used to identify drug resistance in
CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the
CC subsequent identification of proteins encoded by it will help to expand
CC our understanding of parasite biology, a process hampered by the
CC complexity of the parasitic lifecycle, and provide new targets for
CC vaccine and drug development. Parasite resistance to drugs and mosquito
CC resistance to insecticides have led to a resurgence of malaria in many
CC parts of the world, and there is a pressing need for vaccines and new
CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide
CC and protein sequences given in the present invention, but which are not
CC specifically mentioned within the specification.
XX
SQ Sequence 11922 BP; 5402 A; 948 C; 1343 G; 4229 T; 0 other;

Query Match 9.4%; Score 46; DB 21; Length 11922;
Best Local Similarity 55.0%; Pred. No. 0.19;

Matches 88; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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Qy    331 TCTTTATAATAAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATAT 390
          | |  |||||   |  ||  |||| |||||||  | | ||||   ||          | |
Db   8019 TTTACATAATTTTAAAAATGAAATTAAATGCATGAAATATATAAACCTTACACAAAGTTT 8078

Qy    391 ATATGACTCAATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACA 450
          ||||||   || ||   |  ||  ||  | ||| |  |  | ||| |||     ||||||
Db   8079 ATATGATGTAAAATACAGATTATTGTTATTGTTTTATAAATTTATAATAATACTTAAACA 8138

Qy    451 TCAATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
          | || || || |   |  |  |||  | | ||||  || ||
Db   8139 TAAAGAATTATTACAGAATGAAAATTATATAAAAGAAGAA 8178
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Job time : 287.089 secs

GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7		125.2	25.6	496	8	AB020613	AB020613 Vigna rad
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9		114	23.3	456	8	PSPI39	X52224 P.sativum p
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c 11		52	10.6	234112	3	PFMAL4P2	AL035475 Plasmodiu
12		50.4	10.3	253305	3	PFMAL3P7	AL034559 Plasmodiu
13		49.8	10.2	8622	8	YSCMTCYTOC	M97514 Saccharomyc
14		49.6	10.1	152409	2	PFMAL1P1	AL031744 Plasmodiu
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18		48.8	10.0	178273	2	AC005308	AC005308 Plasmodiu
c 19		48.6	9.9	9963	6	AX345596	AX345596 Sequence
c 20		48.4	9.9	206059	2	AC127383	AC127383 Homo sapi
c 21		48.2	9.8	93491	2	AC116967	AC116967 Dictyoste
c 22		48.2	9.8	179075	2	AC018518	AC018518 Homo sapi
23		48	9.8	163443	2	AC006280	AC006280 Plasmodiu
24		47.8	9.8	133501	2	AC116956	AC116956 Dictyoste
25		47.8	9.8	147419	2	AC091835	AC091835 Homo sapi
c 26		47.8	9.8	162608	9	AC009478	AC009478 Homo sapi
c 27		47.6	9.7	156060	2	AC004153	AC004153 Plasmodiu
c 28		47.6	9.7	161508	2	AL772329	AL772329 Danio rer
29		47.6	9.7	169794	2	AC004688	AC004688 Plasmodiu
c 30		47.4	9.7	2459	3	AF205581	AF205581 Plasmodiu
c 31		47.2	9.6	12240	3	AE001424	AE001424 Plasmodiu
32		47	9.6	321003	2	PFMAL4P3	AL035476 Plasmodiu
33		46.8	9.6	14923	3	AE001394	AE001394 Plasmodiu
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35		46.6	9.5	31938	2	AC131427	AC131427 Rattus no
36		46.6	9.5	66441	3	PFMAL1P4	AL031747 Plasmodiu
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c 38		46.6	9.5	160033	2	AC094845	AC094845 Rattus no
c 39		46.6	9.5	203348	9	AC104376	AC104376 Homo sapi
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41		46.2	9.4	153477	2	AC006278	AC006278 Plasmodiu
c 42		46	9.4	6169	6	AX251124	AX251124 Sequence
c 43		46	9.4	6169	6	AX344689	AX344689 Sequence
c 44		46	9.4	6557	6	AX345903	AX345903 Sequence
c 45		46	9.4	17470	3	AE001402	AE001402 Plasmodiu

ALIGNMENTS

RESULT 1
AF319468
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF319468
VERSION AF319468.1 GI:11762085
KEYWORDS .
SOURCE Medicago sativa.
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 406)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakimi,S.

```
  TITLE     Antifungal Polypeptide(s) and Methods for Controlling Plant
            Pathogenic Fungi
  JOURNAL   Patent: US 6121436 19-SEP-2000;
            Monsanto Company; St Louis, MO
REFERENCE   2  (bases 1 to 406)
  AUTHORS   Gao,A.G., Hakimi,S.M., Mittanck,C.A., Wu,Y., Woerner,B.M.,
            Stark,D.M., Shah,D.M., Liang,J. and Rommens,C.M.
  TITLE     Fungal pathogen protection in potato by expression of a plant
            defensin peptide
  JOURNAL   Nat. Biotechnol. 18 (12), 1307-1310 (2000)
  MEDLINE   20553844
   PUBMED   11101813
REFERENCE   3  (bases 1 to 406)
  AUTHORS   Mittanck,C.A., Wu,Y., Hakimi,S.M., Liang,J., Shah,D.M. and Gao,A.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway,
            St Louis, MO 63198, USA
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     mat_peptide     156. .290
                     /product="antifungal protein"
BASE COUNT      140 a     74 c     78 g    114 t
ORIGIN

  Query Match           82.9%;  Score 406;  DB 8;  Length 406;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-74;
  Matches  406;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60

Qy      61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
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Qy     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180

Qy     181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240

Qy     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300

Qy     301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360

Qy     361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCG 406
          |||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCG 406


RESULT 2
PEADRR230A
LOCUS       PEADRR230A              468 bp    mRNA    linear   PLN 11-FEB-2002
DEFINITION  Pea (pi230) disease resistance response protein 230 (DRR230-a)
            mRNA, complete cds.
ACCESSION   L01578 S88685
VERSION     L01578.1  GI:169073
KEYWORDS    cysteine-rich protein; disease resistance response protein 230;
            pathogenesis-related protein.
SOURCE      Pisum sativum.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
   PUBMED   1799696
COMMENT     On Feb 8, 2002 this sequence version replaced gi:247416.
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Pisum sativum"
                     /strain="Alaska"
                     /db_xref="taxon:3888"
                     /tissue_type="pod tissue treated with Fusarium solani
                     conidia"
                     /dev_stage="immature"
     gene            1. .468
                     /gene="DRR230-a"
     CDS             78. .296
                     /gene="DRR230-a"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /note="pi230"
                     /codon_start=1
                     /evidence=experimental
                     /product="disease resistance response protein"
                     /protein_id="AAA79117.1"
                     /db_xref="GI:169074"
                     /translation="MEKKSLACLSFLLLVLFVAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
     mat_peptide     159. .293
                     /gene="DRR230-a"
                     /product="disease resistance response protein"
                     /function="unknown"
                     /note="determined by in vitro cleavage with microsomal
                     membranes"
                     /evidence=experimental
BASE COUNT      153 a     88 c     84 g    143 t
ORIGIN

  Query Match           42.4%;  Score 208;  DB 8;  Length 468;
  Best Local Similarity   72.2%;  Pred. No. 2.3e-33;
  Matches  345;  Conservative    0;  Mismatches  112;  Indels   21;  Gaps    5;

Qy       4 CAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAAT 63
          || | |||||||||||||| |      |||||||||   | | | ||||||||||| |
Db       6 CACAAACACACATAACACATTAAGTGAAGTGAGTCATATTAAGTTTTTATATTCATCACT 65

Qy      64 -CTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTC 122
           || |  || | ||||||||||||||||||||| |||| | ||||||| || | ||||||
Db      66 ACTTAAGAAGCCATGGAGAAGAAATCACTAGCTTGCTTGTCCTTCCTCCTCCTCGTTCTC 125

Qy     123 TTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAA 182
           |||||||||||||||| |||||||  |||| |  ||||||||||||||||| | |  |
Db     126 TTTGTTGCACAAGAAATAGTGGTGAGTGAAGCAAACACATGTGAGAATTTGGCTGGTTCA 185

Qy     183 TATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTT 242
           |||| ||||  ||||||  |||| ||||||  |||||| | |||  |||||  |||| ||
Db     186 TATAAGGGAGTATGCTTCGGTGGATGTGACCGTCACTGTAGAACACAAGAGGGCGCAATT 245

Qy     243 AGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTC 302
           || || || || ||||| ||||| ||||| ||||| |||||||  ||||||||   | |
Db     246 AGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGCACTAAAAACTGTTAAATCCCTTTT 305
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Qy    303 CTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCA 362
          |||||||| ||| |     |     ||| |   ||||||| || |||||||| |
Db    306 CTCCAACACCAACAACACCCATATATAAT-ACTATAATATAAATAAATAAACA------- 357

Qy    363 CGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGT 422
            |  | |    |    ||||| | | | |||||||||||| | ||||||| || ||
Db    358 ------AGTGTTGTTTCGAATTCTATGTGTGT-ACTCAATATCGTGTATAACGTGTTTGT 410

Qy    423 TATGCACTT-----CTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAA 475
          |||||||||      |||||||||||||||| |  ||| | | ||||| | |||||||
Db    411 TATGCACTTTTATCATATCATATGGAATAAAAAGTAATCAATCATTTCCTTTCCAAAA 468


RESULT 3
PSPI230
LOCUS       PSPI230                   468 bp    mRNA    linear   PLN 09-AUG-2002
DEFINITION  P.sativum pI230 mRNA.
ACCESSION   X52225
VERSION     X52225.1  GI:22208748
KEYWORDS    secreted protein.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
REFERENCE   2  (bases 1 to 468)
  AUTHORS   Chiang,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1990) Chiang C., Washington State University,
            Dept. of Plant Phatology, Pullman, WA 99164-6430, USA
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Pisum sativum"
                     /db_xref="taxon:3888"
                     /tissue_type="endocarp"
     gene            1. .468
                     /gene="pI230"
     CDS             78. .296
                     /gene="pI230"
                     /codon_start=1
                     /protein_id="CAA36474.1"
                     /db_xref="GI:22208749"
                     /translation="MEKKSLACLSFLLLVLFVAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
     sig_peptide     78. .158
                     /gene="pI230"
     mat_peptide     159. .293
                     /gene="pI230"
                     /product="unnamed"
BASE COUNT      153 a     88 c     84 g    143 t
ORIGIN

  Query Match           42.4%;  Score 208;  DB 8;  Length 468;
  Best Local Similarity   72.2%;  Pred. No. 2.3e-33;
  Matches  345;  Conservative    0;  Mismatches  112;  Indels   21;  Gaps    5;

Qy      4 CAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAAT 63
          || | |||||||||||||| |      |||||||||   |  | | ||||||||||| |
Db      6 CACAAACACACATAACACATTAAGTGAAGTGAGTCATATTAAGTTTTTATATTCATCACT 65

Qy     64 -CTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTC 122
           || |  || | |||||||||||||||||||| |||| | ||||||| || | ||||||
Db     66 ACTTAAGAAGCCATGGAGAAGAAATCACTAGCTTGCTTGTCCTTCCTCCTCCTCGTTCTC 125

Qy    123 TTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAA 182
          |||||||||||||||| |||||||  ||||| |  |||||||||||||||| | |  |
Db    126 TTTGTTGCACAAGAAATAGTGGTGAGTGAAGCAAACACATGTGAGAATTTGGCTGGTTCA 185

Qy    183 TATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTT 242
          |||| |||  ||||||  |||| ||||||  |||||| | |||  |||||  |||| ||
Db    186 TATAAGGGAGTATGCTTCGGTGGATGTGACCGTCACTGTAGAACACAAGAGGGCGCAATT 245

Qy    243 AGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTC 302
          || || || || ||||| ||||| ||||| ||||| |||||||  ||||||||   | |
Db    246 AGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGCACTAAAAACTGTTAAATCCCTTTT 305

Qy    303 CTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCA 362
          |||||||| ||| |     |     ||| |   ||||||| || |||||||| |
Db    306 CTCCAACACCAACAACACCCATATATAAT-ACTATAATATAAATAAATAAACA------- 357

Qy    363 CGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGT 422
            |  | |    |    ||||| | | | |||||||||||| | ||||||| || ||
Db    358 ------AGTGTTGTTTCGAATTCTATGTGTGT-ACTCAATATCGTGTATAACGTGTTTGT 410

Qy    423 TATGCACTT-----CTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAA 475
          |||||||||      |||||||||||||||| |  ||| | | ||||| | |||||||
Db    411 TATGCACTTTTATCATATCATATGGAATAAAAAGTAATCAATCATTTCCTTTCCAAAA 468


RESULT 4
AF139018
LOCUS       AF139018                  363 bp    mRNA    linear   PLN 02-JAN-2001
DEFINITION  Pisum sativum disease resistance response protein 230 precursor
            (DRR230) mRNA, complete cds.
ACCESSION   AF139018
VERSION     AF139018.1  GI:12002298
KEYWORDS    .
SOURCE      Pisum sativum.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Savenstrand,H., Brosche,M. and Strid,A.
  TITLE     Stress-induced disease resistance response protein 230 cDNA from
            Pisum sativum cv. Greenfeast
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Savenstrand,H., Brosche,M. and Strid,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg
            University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Pisum sativum"
                     /cultivar="Greenfeast"
                     /db_xref="taxon:3888"
     gene            1. .363
                     /gene="DRR230"
     CDS             56. .274
                     /gene="DRR230"
                     /note="ozone-induced; similar to the Pisum sativum cv.
                     Alaska product encoded by GenBank Accession Number L01578"
                     /codon_start=1
                     /product="disease resistance response protein 230
                     precursor"
                     /protein_id="AAG43285.1"
                     /db_xref="GI:12002299"
                     /translation="MEKKSLACLSFLLLVLFIAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
BASE COUNT      113 a     68 c     74 g    108 t
ORIGIN

  Query Match           35.8%;  Score 175.6;  DB 8;  Length 363;
  Best Local Similarity   75.2%;  Pred. No. 1.2e-26;
  Matches  245;  Conservative    0;  Mismatches   79;  Indels    2;  Gaps    2;
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Qy      32 GTGAGTCATTAAATTTATATATATTCATCAAT-CTAATCAAACTATGGAGAAGAAATCAC 90
           |||||||||   |  | |  |||||||||| | ||  |   ||  | ||||||||||||||||
Db      12 GTGAGTCATATTAAGTTTTGATATTCATCACTACTTAAGAAGCCATGGAGAAGAAATCAC 71

Qy      91 TAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAG 150
           ||||| |||| | ||||||| || | |||||||||| |||||||||||| |||||||  |
Db      72 TAGCTTGCTTGTCCTTCCTCCTCCTCGTTCTCTTTATTGCACAAGAAATAGTGGTGAGTG 131

Qy     151 AAGCCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTG 210
           ||||  |  |||||||||||||||| | |  ||||| ||||  ||||||  |||| ||||
Db     132 AAGCAAACACATGTGAGAATTTGGCTGGTTCATATAAGGGAGTATGCTTCGGTGGATGTG 191

Qy     211 ACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCT 270
           ||  |||||| | |||  |||||  ||||  |||| || || || |||||  |||||  ||||
Db     192 ACCGTCACTGTAGAACACAAGAGGGCGCAATTAGCGGCAGATGCAGGGATGACTTTCGCT 251

Qy     271 GCTGGTGTACTAAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAG 330
           | |||||  |||||||  ||||||||    | | |||||||| ||| |    |      | |
Db     252 GTTGGTGCACTAAAAACTGTTAAATCCCTTTTCTCCAACACCAACAACACCCATATAGAA 311

Qy     331 TCTTTATAATAAAACTAAATAAATAA 356
           |   ||||||| || ||||||||  ||
Db     312 T-ACTATAATATAAATAAATAAACAA 336


RESULT 5
AX252303
LOCUS       AX252303                494 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168887.
ACCESSION   AX252303
VERSION     AX252303.1  GI:15985643
KEYWORDS    .
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   Jung,R. and Kinney,A.J.
  TITLE     Hypoallergenic transgenic soybeans
  JOURNAL   Patent: WO 0168887-A 5 20-SEP-2001;
            E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
            INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .494
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
BASE COUNT      153 a     97 c    103 g    134 t      7 others
ORIGIN

  Query Match             26.0%;  Score 127.4;  DB 6;  Length 494;
  Best Local Similarity   68.4%;  Pred. No. 1.2e-16;
  Matches  225;  Conservative    0;  Mismatches   91;  Indels   13;  Gaps    3;

Qy      46 TTATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCT 105
           |||  |||  |          |||||  || | |||||||||||||||| |||||||  || ||||
Db      17 TTACATACACGTGAATCACTAATTAAGCCATGGAGAAGAAATCAATAGCTGGGTTGTGCT 76

Qy     106 TCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACAT 162
           ||||||||  | ||||||||||||||  ||||||  ||||||||    || || || |   || |
Db      77 TCCTCTTCCTTGTTCTCTTTGTTGCTCAAGAAGTTGTGGTGCAAACTGAGGCAAAGACTT 136

Qy     163 GTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTC 216
           | |||||  ||||  ||||  |||  |||||  ||||||||       |  |  | ||  ||   ||
Db     137 GCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGATGATC 196

Qy     217 ACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
           ||||||  | |||||||  ||    | || ||  ||  || ||||||||  || |||||  ||||
Db     197 ACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGTTGGT 256

Qy     277 GTACTAAAAGATGTTAAATGGATC----TCCTCCAACATCAAGATGTGCATGGAATAGTC 332
           | || ||||  ||||||||||||||      |||||||  | ||||  |      | |  |
Db     257 GCACCAAAAACTGTTAAATGGATCCATTCACTCCAACGTGAAGAAGATGCATGCAGCGCT 316

Qy     333 TTTATAATAAAACTAAATAAATAAAATGC 361
           ||  ||  |||| || |    |  | || |
Db     317 ATTTTATAAAAAATACAACTACTATATAC 345


RESULT 6
VUSTORED
LOCUS       VUSTORED                459 bp    mRNA    linear   PLN 12-SEP-1993
DEFINITION  Vigna unguiculata cDNA for stored cotyledon mRNA.
ACCESSION   X16877
VERSION     X16877.1  GI:22075
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Yamauchi,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo
            Metropolitan University, Fukazawa 2-1, Setagaya-ku, Tokyo 158,
            Japan
REFERENCE   2  (bases 1 to 459)
  AUTHORS   Ishibashi,N., Yamauchi,D. and Minamikawa,T.
  TITLE     Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide
            sequence of cloned cDNA for a stored mRNA and induction of its
            synthesis by precocious germination
  JOURNAL   Plant Mol. Biol. 15 (1), 59-64 (1990)
  MEDLINE   91355865
   PUBMED   2103443
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Vigna radiata"
                     /db_xref="taxon:157791"
                     /clone="pSAS10"
                     /tissue_type="cotyledon"
                     /clone_lib="lambda gt10"
                     /dev_stage="seed"
     CDS             14. .241
                     /note="pSAS10 ORF"
                     /codon_start=1
                     /protein_id="CAA34760.1"
                     /db_xref="GI:22076"
                     /db_xref="SWISS-PROT:P18646"
                     /translation="MEKKSIAGLCFLFLVLFVAQEVVVQSEAKTCENLVDTYRGPCFT
                     TGSCDDHCKNKEHLLSGRCRDDVRCWCTRNC"
BASE COUNT      136 a     91 c     99 g    133 t
ORIGIN

  Query Match             25.8%;  Score 126.2;  DB 8;  Length 459;
  Best Local Similarity   68.9%;  Pred. No. 2.1e-16;
  Matches  235;  Conservative    0;  Mismatches   93;  Indels   13;  Gaps    4;

Qy      64 CTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCT 123
           ||||  || | |||||||||||||||| | ||||| |||||||||||||||| | |||||||
Db       3 CTAAATAAGCCATGGAGAAGAAATCAATCGCTGGATTATGCTTCCTCTTCCTTGTTCTCT 62

Qy     124 TTGTTGCACAAGAAATTGTGGT---GACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
           |||||||  ||||||  |||||||    ||  || || |  || || |||||  |||  ||||
Db      63 TTGTTGCTCAAGAAGTTGTGGTGCAGAGTGAGGCAAAGACTTGCGAGAACCTGGTGGATA 122

Qy     181 AATATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTGCACAACCAAAGAGA 234
           |||  |||||  || |||||       |  |  | ||:||   ||||||||  | ||||||
Db     123 CATACAGGGGTCCGTGCTTCACCACTGGGAGCTGCGATGATCACTGCAAGAACAAAGAAC 182

Qy     235 ACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAA 294
           ||    | |||||  |||||  |||||  ||  ||||.||  |||||  || |  ||  ||||||
Db     183 ACTTGCTGAGTGGCAGGTGCAGGGATGATGTCCGGTGTTGGTGCACCAGAAACTGTTAAC 242
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Qy    295 TGGATCTCCTCCAA---CATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATA 351
          |||||  ||||||    |   | | ||||||| |      |||||||  |||  ||  |
Db    243 TGGATTCTCTCCAAACCTAGACAAACGTGCATGCAGGGCATTTTATAAATAAAACAACCA 302

Qy    352 AATAAAATGCACGCAGTATAGCTACAACTTCATCTATATAT 392
           || | ||  |  || ||   || | ||| ||||||||||
Db    303 TAT-ATATATATACAATAAGCCTTCTACTGCATCTATATAT 342


RESULT 7
AB020613
LOCUS       AB020613                496 bp    mRNA    linear   PLN 05-JAN-2002
DEFINITION  Vigna radiata mRNA for PDF1, complete cds.
ACCESSION   AB020613
VERSION     AB020613.1  GI:18146787
KEYWORDS    PDF1.
SOURCE      Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA,
            clone_lib:B20 clone:pDF-1.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1
  AUTHORS   Ishimoto,M. and Kaga,A.
  TITLE     Mungbean defensin
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 496)
  AUTHORS   Ishimoto,M. and Kaga,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National
            Agricultural Experiment Station, Laboratory of Plant Biotechnology;
            6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan
            (E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231),
            Fax:+81-849-247893)
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Vigna radiata"
                     /strain="B20F5 9-3-2-2"
                     /db_xref="taxon:157791"
                     /clone="pDF-1"
                     /tissue_type="immature seed"
                     /clone_lib="B20"
     gene            1. .496
                     /gene="pDF1"
     CDS             46. .273
                     /gene="pDF1"
                     /codon_start=1
                     /product="PDF1"
                     /protein_id="BAB82453.1"
                     /db_xref="GI:18146788"
                     /translation="MEKKSLAGLCFLFLVLFVAQEVMVQTEAKTCENLANTYRGPCFT
                     TGSCDDHCKNKEHLRSGRCRDDFRCWCTRNC"
     polyA_site      496
                     /gene="pDF1"
                     /note="17 a nucleotides"
BASE COUNT      148 a    104 c    106 g    138 t
ORIGIN

  Query Match             25.6%;  Score 125.2;  DB 8;  Length 496;
  Best Local Similarity   66.7%;  Pred. No. 3.3e-16;
  Matches  228;  Conservative    0;  Mismatches  103;  Indels   11;  Gaps    3;

Qy     64 CTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCT 123
          ||||  || | ||||||||||||||||| || || |||||||||||||| | |||||||
Db     35 CTAACTAAGCCATGGAGAAGAAATCACTGGCCGGATTATGCTTCCTCTTCCTTGTTCTCT 94

Qy    124 TTGTTGCACAAGAAATTGTGGT---GACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
          ||||||| |||||| || ||||   ||| || || |  || || |||||  ||||  |||
Db     95 TTGTTGCTCAAGAAGTTATGGTGCAGACTGAGGCAAAGACTTGCGAGAACCTGGCGAATA 154

Qy    181 AATATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTGCACAACCAAAGAGA 234
          || ||||| |||||||||   .  | |  | || ||   ||||||||  | ||||||
Db    155 CTTACAGGGGTCCATGCTTCACCACTGGCAGCTGCGATGATCACTGCAAGAACAAAGAAC 214

Qy    235 ACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAA 294
          ||      ||||| ||||| |||||||| ||||| || ||||| |||| ||  ||||||
Db    215 ACTTGAGGAGTGGCAGGTGCAGGGACGATTTCCGGTGTTGGTGCACTAGAAACTGTTAAC 274

Qy    295 TGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAAT 354
          ||||   | |||||   || |   |          | | || ||   |||  ||| |
Db    275 CGGATTCTCCCCAACCCGAACAAACGTGCATGCAGGGCATTTTA--TAAATAAAAAACTA 332

Qy    355 AAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGA 396
          | || ||  || ||   || | ||| ||| | ||||| | |
Db    333 TATATACATACAATAAGCCTTCTACTGCATATCTATATGTCA 374


RESULT 8
PEADRR230B
LOCUS       PEADRR230B              456 bp    mRNA    linear   PLN 11-FEB-2002
DEFINITION  Pisum sativum disease resistance response protein 39 (DRR230-b)
            mRNA, complete cds.
ACCESSION   L01579 S88682
VERSION     L01579.1  GI:169075
KEYWORDS    cysteine-rich protein; disease resistance response protein 39;
            pathogenesis-related protein.
SOURCE      Pisum sativum (strain Alaska) cDNA to mRNA.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
   PUBMED   1799696
COMMENT     On Feb 8, 2002 this sequence version replaced gi:247414.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Pisum sativum"
                     /strain="Alaska"
                     /db_xref="taxon:3888"
                     /tissue_type="pod tissue treated with Fusarium solani
                     conidia."
                     /dev_stage="immature"
     gene            1. .456
                     /gene="DRR230-b"
     CDS             69. .293
                     /gene="DRR230-b"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /codon_start=1
                     /evidence=experimental
                     /product="disease resistance response protein 39"
                     /protein_id="AAA79118.1"
                     /db_xref="GI:169076"
                     /translation="MEKKSLAALSFLLLLVLFVAQEIVVTEANTCEHLADTYRGVCFT
                     NASCDDHCKNKAHLISGTCHDWKCFCTQNC"
     mat_peptide     153. .290
                     /gene="DRR230-b"
                     /product="disease resistance response protein"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /note="citocleavage determined by homology with pi230;
                     putative"
BASE COUNT      155 a     81 c     79 g    141 t
ORIGIN

  Query Match             23.3%;  Score 114;  DB 8;  Length 456;
  Best Local Similarity   61.4%;  Pred. No. 6.9e-14;
  Matches  277;  Conservative    0;  Mismatches  151;  Indels   23;  Gaps    5;
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Qy      9 ACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAATC--TA 66
          | ||||| |||| || |      |||| ||||  |  |  || || |  ||  |||   |
Db      1 AAACACACAACATATTAAGTGAAGTGAATCATATATATATTAAATCTATATTCATCATCA 60

Qy     67 ATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTG---GTTCTCT 123
           | ||  |||||||||||||||||||||||| ||| | |||||| || |    |||||||
Db     61 CTAAAGTTATGGAGAAGAAATCACTAGCTGCCTTGTCCTTCCTCCTCCTCCTCGTTCTCT 120

Qy    124 TTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAAT 183
          |||||||||||||||||||||||||||||| || |  || |||||| ||||||| |||| ||
Db    121 TTGTTGCACAAGAAATTGTGGTGACAGAGGCAAACACTTGTGAGCATTTGGCTGATACAT 180

Qy    184 ATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACG 237
          | ||||||  ||||||      |  | | |||||   |||||||  | ||||| | ||
Db    181 ACAGGGGAGTATGCTTCACGAATGCTAGCTGTGATGATCACTGCAAGAACAAAGCGCACT 240

Qy    238 CAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGG 297
          | | ||||| | ||   |  | ||||     || |  || ||| |||  |||||||
Db    241 TAATCAGTGGCACGT---GCCATGACTGGAAATGTTTCTGCACTCAAAACTGTTAAA--- 294

Qy    298 ATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAA 357
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Db    295 ------GACGTTATAAGTATAATAATATAAATAAATAAAATGCATGCAGTTATAGCAACT 348

Qy    358 ATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTA 417
          |    | |     |    | || |   |  ||| ||  |    |||| | ||||| ||
Db    349 ACCGCTGTATCTGTGTATGTATTTGAATAAGTTATGTGTGTACTCATCGTGTATAACCTA 408

Qy    418 TTAGTTATGCACTTCTATCATATGGAATAAA 448
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Db    409 CTAGTTATGCACTTTTATCTTATGGAATAAA 439


RESULT 9
PSPI39
LOCUS       PSPI39                   456 bp    mRNA    linear   PLN 09-AUG-2002
DEFINITION  P.sativum pI39 mRNA.
ACCESSION   X52224
VERSION     X52224.1  GI:22208744
KEYWORDS    secreted protein.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
REFERENCE   2  (bases 1 to 456)
  AUTHORS   Chiang,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1990) Chiang C., Washington State University,
            Dept. of Plant Phatology, Pullman, WA 99164-6430, USA
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Pisum sativum"
                     /db_xref="taxon:3888"
                     /tissue_type="endocarp"
     gene            1. .456
                     /gene="pI39"
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                     /db_xref="GI:22208745"
                     /translation="MEKKSLAALSFLLLLVLFVAQEIVVTEANTCEHLADTYRGVCFT
                     NASCDDHCKNKAHLISGTCHDWKCFCTQNC"
     sig_peptide     69. .152
                     /gene="pI39"
     mat_peptide     153. .290
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BASE COUNT      155 a     81 c     79 g    141 t
ORIGIN

  Query Match           23.3%;  Score 114;  DB 8;  Length 456;
  Best Local Similarity   61.4%;  Pred. No. 6.9e-14;
  Matches  277;  Conservative    0;  Mismatches  151;  Indels   23;  Gaps    5;

Qy      9 ACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAATC--TA 66
          | ||||| |||| || |      |||| ||||  |  |  || || |  ||  |||   |
Db      1 AAACACACAACATATTAAGTGAAGTGAATCATATATATATTAAATCTATATTCATCATCA 60

Qy     67 ATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTG---GTTCTCT 123
           | ||  |||||||||||||||||||||||| ||| | |||||| || |    |||||||
Db     61 CTAAAGTTATGGAGAAGAAATCACTAGCTGCCTTGTCCTTCCTCCTCCTCCTCGTTCTCT 120

Qy    124 TTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAAT 183
          |||||||||||||||||||||||||||||| || |  || |||||| ||||||| |||| ||
Db    121 TTGTTGCACAAGAAATTGTGGTGACAGAGGCAAACACTTGTGAGCATTTGGCTGATACAT 180

Qy    184 ATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACG 237
          | ||||||  ||||||      |  | | |||||   |||||||  | ||||| | ||
Db    181 ACAGGGGAGTATGCTTCACGAATGCTAGCTGTGATGATCACTGCAAGAACAAAGCGCACT 240

Qy    238 CAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGG 297
          | | ||||| | ||   |  | ||||     || |  || ||| |||  |||||||
Db    241 TAATCAGTGGCACGT---GCCATGACTGGAAATGTTTCTGCACTCAAAACTGTTAAA--- 294

Qy    298 ATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAA 357
              |   || |  ||    ||  ||     | |    |       |||   |
Db    295 ------GACGTTATAAGTATAATAATATAAATAAATAAAATGCATGCAGTTATAGCAACT 348

Qy    358 ATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTA 417
          |    | |     |    | || |   |  ||| ||  |    |||| | ||||| ||
Db    349 ACCGCTGTATCTGTGTATGTATTTGAATAAGTTATGTGTGTACTCATCGTGTATAACCTA 408

Qy    418 TTAGTTATGCACTTCTATCATATGGAATAAA 448
          |||||||||||| |||| ||||||||||
Db    409 CTAGTTATGCACTTTTATCTTATGGAATAAA 439


RESULT 10
AB049718/c
LOCUS       AB049718                 380 bp    mRNA    linear   PLN 08-JUN-2001
DEFINITION  Pisum sativum ssa-8 mRNA for putative senescence-associated
            protein, complete cds.
ACCESSION   AB049718
VERSION     AB049718.1  GI:13359440
KEYWORDS    .
SOURCE      Pisum sativum (cultivar:Ichihara wase) immatured pods pods cDNA to
            mRNA.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (sites)
  AUTHORS   Pariasca,J.A.T., Sunaga,A., Miyazaki,T., Hisaka,H., Sonoda,M.,
            Nakagawa,H. and Sato,T.
  TITLE     Cloning of cDNAs encoding senescence-associated genes, ACC synthase
            and ACC oxidase from stored snow pea pods (Pisum sativum L. var
            saccharatum) and their expression during pod storage
  JOURNAL   Postharvest Biology and Technology 22, 239-247 (2001)
REFERENCE   2  (bases 1 to 380)
  AUTHORS   Pariasca,J.A. and Sato,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-2000) Takahide Sato, Chiba University, Faculty of
            Horticulture; 648 Matsudo, Matsudo, Chiba 271-8510, Japan
            (E-mail:sato@midori.h.chiba-u.ac.jp, Tel:81-47-308-8863)
FEATURES             Location/Qualifiers
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     source          1. .380
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                     /cultivar="Ichihara wase"
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                     /tissue_type="pods"
                     /dev_stage="immatured pods"
                     /country="Japan: Chiba, Matsudo"
                     /note="cDNAs isolated from a 5-day stored pod cDNA library
                     by differential screening"
     gene            1. .380
                     /gene="ssa-8"
     CDS             98. .370
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                     /codon_start=1
                     /product="putative senescence-associated protein"
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                     /db_xref="GI:13359441"
                     /translation="MHDIEYTHNSQSRIQHTGAVQILHIIVFIHIIWSFIFLHILSLR
                     VGENWINSFECTSSENHPCTSHSVCARCSCNVCCSYHLGCMVPVFY"
BASE COUNT      120 a     78 c     64 g    118 t
ORIGIN

  Query Match             11.3%;  Score 55.2;  DB 8;  Length 380;
  Best Local Similarity   67.2%;  Pred. No. 0.11;
  Matches   78;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy     200 TAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGA 259
           | ||   ||  |||  || ||||  | ||| ||| ||  | | ||||| ||||| |||||
Db     339 TGGTAACTGCAACAAACATTGCAGGAACAACGAGCACATACTGAGTGGGAGGTGCAGGGA 280

Qy     260 CGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTCCTCCAACATCAAG 315
           || || ||||||||||| |||  ||  ||||||     | | ||||||||   ||
Db     279 TGATTTTCGCTGCTGGTGCACTCGAAACTGTTAATCCAGTTTTCTCCAACACGCAG 224


RESULT 11
PFMAL4P2/c
LOCUS       PFMAL4P2              234112 bp    DNA     linear   INV 31-MAY-2000
DEFINITION  Plasmodium falciparum MAL4P2, complete sequence.
ACCESSION   AL035475
VERSION     AL035475.6  GI:6562702
KEYWORDS    HTG; DNA polymerase alpha; DnaJ; flap exonuclease; protein
            phosphatase; replication A protein; ribosomal processing protein;
            ribosomal protein; rifin; transcription factor; var.
SOURCE      Plasmodium falciparum 3D7.
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 234112)
  AUTHORS   Devlin,K., Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D.,
            Quail,M. and Barrell,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
            The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA, UK
COMMENT     On Dec 12, 1999 this sequence version replaced gi:5731898.
            For more information about this sequence or the Malaria Project,
            see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This
            sequence is not the entire insert of clone MAL4P2. It may be
            shorter because we only sequence overlapping sections once, or
            longer because we arrange for a small overlap between neighbouring
            submissions.
FEATURES            Location/Qualifiers
     source         1. .234112
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                    /db_xref="taxon:36329"
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                    /gene="MAL4P2.01"
     CDS            complement(1. .3390)
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                    /gene="MAL4P2.01"
                    /note="MAL4P2.01, hypothetical protein, partial orf, len:
                    > 1130 aa, contains NKSKPDD repeat sequence"
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                    EQMDIHKYMYTHKYTHYEIYKSMFAYGKIAQMRNNLEIMKCRISIEQIENELEKKKIQ
                    REIMFIEEQKEKMKEEKIFIEEEKKKIKDQKIYIDEENKKMNTERLIIDLEQINHEQT
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                    10170. .10250,10340. .10378,10551. .10706,10776. .10787)
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                    /note="MAL4P2.03, hypothetical protein, len: 853 aa, 13
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                    NETLHKNIEDLHQEKSYLKKELELLKKDHIEKLNEKELTIGTLNDLVNSSHEKQIKAD
                    EQYEEIKKLIEENQKEYSQQIKKKEESLDYIRNISTMLHNKCYPKYMINFDQIPFYQA
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/note="predicted splice donor sequence, caa/gtaaat, for exon 2 of MAL4P2.03"

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/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 3 of MAL4P2.03"

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misc_feature 7556. .7565
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 4 of MAL4P2.03"

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/note="predicted splice donor sequence, aac/gtttgt, for exon 4 of MAL4P2.03"

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/note="predicted splice acceptor sequence for exon 5 of MAL4P2.03"

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/note="potential splice donor sequence, caa/gtaaaa, for exon 5 of MAL4P2.03"

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misc_feature 8358. .8363
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/note="potential splice donor sequence, cag/gtagga, for exon 6 of MAL4P2.03"

misc_feature 8443. .8453
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 7 of MAL4P2.03"

misc_feature 8589. .8594
/gene="MAL4P2.03"
/note="predicted splice donor sequence, tat/gtatat, for exon 7 of MAL4P2.03"

misc_feature 8628. .8637
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 8 of MAL4P2.03"

misc_feature 9610. .9615
/gene="MAL4P2.03"
/note="predicted splice donor sequence, acc/gtaaat, for exon 8 of MAL4P2.03"

misc_feature 9645. .9650
/gene="MAL4P2.03"
/note="alternative splice donor sequence, acc/gtaaat, for exon 8 of MAL4P2.03"

misc_feature 9730. .9739
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 9 f MAL4P2.03"

misc_feature 9747. .9756
/gene="MAL4P2.03"
/note="alternative splice acceptor sequence for exon 9 of MAL4P2.03"

misc_feature 10019. .10024
/gene="MAL4P2.03"
/note="predicted splice donor sequence, cac/gtaaga, for exon 9 of MAL4P2.03"

misc_feature 10160. .10169
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 10 of MAL4P2.03"

misc_feature 10251. .10256
/gene="MAL4P2.03"
/note="predicted splice donor sequence, aag/gtaata, for exon 10 of MAL4P2.03"

misc_feature 10330. .10339
/gene="MAL4P2.03"
/note="predicted splice acceptor sequence for exon 11 of MAL4P2.03"

Query Match 10.6%; Score 52; DB 3; Length 234112;
Best Local Similarity 52.9%; Pred. No. 0.28;
Matches 109; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Qy    282 AAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATA 341
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Db 206930 AAAAAAAAAAAAAAATATATATTGAAAAATATAATTGTTAGAGAAAAAAAATACAAATAA 206871

Qy    342 AAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAA 401
          ||     | ||| |||||  |   |  | |   | ||     |||| | | |  |    |
Db 206870 AATAGCCAAAAAAAAAATTAAAAAAAAAAAAATAATAAAAATTTCTACAAAAACAAAAATA 206811

Qy    402 TATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAA 461
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Db 206810 TATTATACAATGAGAACTATATAGAAATTTAAATAATAAAAAAGAAAAAGGAAAAAATAA 206751

Qy    462 TTTCGTNTCCAAAAAAAAAAAAAAAA 487
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Db 206750 CTTTTTTTCCAAAAAAAAAAAAAAAA 206725
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RESULT 12
PFMAL3P7
LOCUS PFMAL3P7 253305 bp DNA linear INV 22-MAY-2000
DEFINITION Plasmodium falciparum MAL3P7, complete sequence.
ACCESSION AL034559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169
AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888
AL139179 Z98556 Z98557 Z98558
VERSION AL034559.4 GI:8052273
KEYWORDS HTG; 40S Ribosomal protein S3A; acyl transferase;
acylaminoacyl-peptidase; ATP-dependent RNA Helicase; cyclophilin;
elongation factor; F49C12.11-like protein; HesB-like domain
protein; histone H2A variant; kinesin-related protein;
N-acetylglucosamine-1-phosphate transferase; protein kinase; R-CG7
repeat; R-FA3 repeat; rep11; rep20; rifin; RNA-binding protein;
stevor; T-complex protein 1 epsilon subunit; telomere; var.
SOURCE Plasmodium falciparum 3D7.
ORGANISM Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 253305)
AUTHORS Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,
Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T.,
Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,
Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J.,
Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A.,
Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,
Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
Barrell,B.G.
TITLE The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum
JOURNAL Nature 400 (6744), 532-538 (1999)
MEDLINE 99376085
PUBMED 10448855

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REFERENCE   2  (bases 1 to 253305)
  AUTHORS   Oliver,K., Bowman,S., Harris,D., Lawson,D., Quail,M. and Barrell,B.
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 253305)
  AUTHORS   Lawson,D., Bowman,S. and Barrell,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
            The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA, UK
COMMENT     On or before May 14, 2001 this sequence version replaced
            gi:2982540, gi:2982541, gi:2982544, gi:2894453, gi:2894464,
            gi:2982551, gi:2982556, gi:2982558, gi:2982563, gi:2982564,
            gi:2982566, gi:2894491, gi:2982569, gi:2695974, gi:2894502,
            gi:2673766, gi:2894496, gi:2982577, gi:2894588, gi:2894589,
            gi:2982538, gi:2982539, gi:2894380, gi:4725992.
            For more information about this sequence or the Malaria Project,
            see http://www.sanger.ac.uk/Projects/P_falciparum.
FEATURES             Location/Qualifiers
     source          1. .253305
                     /organism="Plasmodium falciparum 3D7"
                     /strain="3D7"
                     /db_xref="taxon:36329"
                     /chromosome="3"
                     /clone="MAL3P7"
     gene            458. .4060
                     /gene="PFC0860w, MAL3P7.1"
     CDS             458. .4060
                     /gene="PFC0860w, MAL3P7.1"
                     /note="PFC0860w (MAL3P7.1), Kinesin-related protein, len:
                     1200 aa; similarity: to kinesin-related protein.
                     D.melanogaster kinesin-like protein 67A (TR:P91945) BLAST
                     Score: 664, sum P(2) = 1.9e-67; 28% identity in 707 aa
                     overlap, predicted using hexExon, Pfam: match to PF00225
                     kinesin, Kinesin motor domain Score 311.54"
                     /codon_start=1
                     /product="kinesin-related protein"
                     /protein_id="CAB39023.1"
                     /db_xref="GI:4493964"
                     /db_xref="SPTREMBL:O97277"
                     /translation="MRKTKNLNDPFFLNNYYYNKEENNPIIICSDEKERKTKIYSTNH
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                     VYPNINGEPSTSVENITNGEHFINGQYDALKNMSLNNYDHQHNNIMNNISNKNKLFVL
                     NNNNNNNNQDVIENMNEYPITSKNIYDSIYIPQINIKNIINSEEINNNNNNINDNNNH
                     NYTNIHNNNNNMNSNPTSSVTSKKNENNNLINTLNAYSNVKVAVRIKPIGESEENIVS
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                     GINCTVFAYGATGSGKTYTMLDDKNQNGIVQLSLLELFTIINEKKCRNIKVLMSFLEV
                     YNETIRDLLGKEKNKTLEVQEDVAEVKVSNLCEIEVNNYEQAMLLINEGVKNRKMSPT
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                     VDENVMVDENVMVDENVMVDENVMVDENVMVNENVVVDKNVSVNENIVVSEKHKVGLS
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                     KKIPINMETKKKRTMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
                     EKKGEYNPFHNNLTDMQNSILYNIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
                     DDDTIKNMNSNKISDKHNMKSNNILNNENGKINDKSKKCKNINNNNNNNNNNNNNNNN
                     NNNNNNNSSSSSSGKVDGINILNNSNTNERLHTFSGVYSLNLNDEIKIEINKKDMEKN
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                     /note="potential splice donor at 3' end of PFCo860w may
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     misc_feature    4057. .4062
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     gene            join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
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     CDS             join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
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                     /note="PFC0865w, (MAL3P7.2), RNA-binding protein, len: 309
                     aa; Similarity eg to C.elegans RNA-binding protein
                     (TR:Q18318) BLAST Score: 378, sum P(1) = 3.8e-35; 37%
                     identity in 297 aa overlap, predicted using hexExon, Pfam:
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                     /db_xref="SPTREMBL:O97318"
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                     LERPLVVDHILNYRLPKKYLKDADKNEYKPTGAEGQGIGVYNVVESEIKLSKVFDKIK
                     NKSNEEKKKKLLDEDELWALNFEKSIKKDIISPIGHDEKSRHNEGMKEEEEDEDDEDD
                     DDEDDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
                     EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
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     CDS             join(7801. .7928,8084. .8234,8392. .8583)
                     /gene="PFC0870w, MAL3P7.3"
                     /note="PFC0870w (MAL3P7.3), putative elongation factor,
                     len: 181 aa; Similarity to P. falciparum elongation factor
                     1-beta, (AAF27524) (276 aa), fasta scores: opt: 366, E():
                     1.1e-15, 53.2% identity in 141 aa overlap, revised:
                     shortened exon 2, Pfam: match to PF00736 EF1BD, EF-1
                     guanine nucleotide exchange domain Score 61.10"
                     /codon_start=1
                     /product="putative elongation factor"
                     /protein_id="CAB39068.2"
                     /db_xref="GI:8052274"
                     /db_xref="SPTREMBL:O97319"
                     /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKKEVINKS
                     SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL
                     VNTDELIETIENLGLDNEQLQKKKQMDDDEENYDEDDEIGGLVQSAEIISFNKL"
     misc_feature    8235. .8240
                     /gene="PFC0870w, MAL3P7.3"
                     /note="revised splice donor sequence for exon 2 of
                     PFC0870w"
     misc_feature    8580. .8585
                     /note="potential splice donor sequence may indicate
                     further splicing of PFC0870w"
     gene            join(11431. .20416,20578. .20690)
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     CDS             join(11431. .20416,20578. .20690)
                     /gene="PFC0875w, MAL3P7.4"
                     /note="PFC0875w (MAL3P7.4), hypothetical protein, len:
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                     end"
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                     /db_xref="SPTREMBL:O97278"
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                     LNDFFIYKMPMKSMKINAFDTFEKNIFRVVVFLCVCLFIVNICFDINKERKINIENFL
                     CCLKINKYYYYYSWLLFYFIILFFYNIIFTLVVYFYVYKCLMNYFILFFLIYFFLMNS
                     LLFTIICMQFSNNSSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
                     LDFIFILIKNNIKIDYKQLFIKFENISLMHLIICSIVSFVLLICILNYIIYYKRKKMN
                     MLNTKYRGKSKSITNDKRKKSQQKTYEYGNINYDMSEKYPTHQLKDNSNDFMLEGSDE
                     DDTCYELDTLHKKQVNSQMCLRIEKIRNDRRESNGHPYDIPMIPLRHNNNINNNINNN
                     INNNINNNINNNINNNQHRNNQCYLIIQNVNKFYGKKHALKDVSLTLRSNRIFVLLGE
                     NGSGKSTLINIITKMISKDSGEINFFKNSYKNKKKDIYMDVNKNRRNGLCGRICSNGY
                     IKEFVMNRIFKRNCNDTNNYDNNSNNNNNNDNHNDNHSNNSGINSSFNNNNNVHNKNI
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                     NDQIKNLMDEVKKKISIFICFLVKRDIYILDEPFIALDIKTKTKLFKFFDKIKKNNII
                     FICTHDIYEANNFANDIAVIKSGQIIFKGSKNSFQKLIEYKFTLNIQFNGLPNEEQTN
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                    NNKNNSVDHIDHLFDILVTNINEFTNNRDIIKKNIIKFIKGTRNENKNCFIFFNENHI
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                    IINSTNHDDNPYDINMYNNHNKYGKYKNNNNNNSFYNMRDDTELTDIEENISSKKKKN
                    KFIEKEFSYNTYRNNKNNDENDEYGEYDNYDDNMIMSNTSNIMKKKNIKKQNIFKTCI
                    NFFTTYIKPTLLLKLKKDLGSSSFYWYKFIVPLFLLSFGLLIIKCVSLFGKVQNIDLD
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                    TKQDDNAEESHINNNDHNDNIKDILKLENNEYNYNKLIHENSFNYYNSTINSLLQKYC
                    LKEKINYIDEPLIEDNLYDSINNYLEKKANHENEISLGTFAFLITEKKADNSDNKEDV
                    ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI
                    ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN
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                    DENNTTMGIYKYGEKVDSNNYISEDEININNQLNSEGYLKNDIYMNELNDNYNNDFDD
                    NTVDIEMQISEKSNIKEKMLYKETEIDKYYKGQSDDDNDEEKNFNKISQKYILKNLNI
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  Query Match            10.3%;  Score 50.4;  DB 3;  Length 253305;
  Best Local Similarity  57.0%;  Pred. No. 0.59;
  Matches   90;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy    333 TTTATAATAAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATAT 392
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Db  64611 TATATAATATAATATTATATATTATTATATATTATTATATATATATATATATATATATAT 64670

Qy    393 ATGACTCAATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATC 452
          || | | |||||    || ||    | |   ||  |  | |||    |  || | |||
Db  64671 ATAAATAAATATTATTCAAAAAAATTAAAAAATAAAAATATATTTGTTTAAAAATACAAA 64730

Qy    453 AATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
          || ||  || ||  |    |||||||||||||| ||||
Db  64731 AAAAAAGAAATTTATTAGAAAAAAAAAAAAAAAATAAAA 64768


RESULT 13
YSCMTCYTOC
LOCUS       YSCMTCYTOC              8622 bp    DNA     linear   PLN 05-MAY-1997
DEFINITION  Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit
            I (COXI) gene, complete cds.
ACCESSION   M97514
VERSION     M97514.1  GI:294042
KEYWORDS    .
SOURCE      Saccharomyces douglasii.
  ORGANISM  Mitochondrion Saccharomyces douglasii
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 8622)
  AUTHORS   Tian,G.L., Michel,F., Macadre,C. and Lazowska,J.
  TITLE     Sequence of the mitochondrial gene encoding subunit I of cytochrome
            oxidase in Saccharomyces douglasii
  JOURNAL   Gene 124 (2), 153-163 (1993)
  MEDLINE   93185919
   PUBMED   8383070
FEATURES             Location/Qualifiers
     source          1. .8622
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                     /db_xref="taxon:46617"
     5'UTR           1. .1152
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                     7896. .7992)
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                     /protein_id="AAB58808.1"
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                     FWVLPMGLVCLVTSTLVESGAGTGWTVYPPLSSIQAHSGPSVDLAIFALHLTSISSLL
                     GAINFIVTTLNMRTNGMTMHKLPLFVWSIFITAFLLLLSLPVLSAGITMLLLDRNFNT
                     SFFEVAGGGDPILYEHLFWFFGHPEVYILIIPGFGIISHVVSTYSKKPVFGEISMVYA
                     MASIGLLGFLVWSHHMYIVGLDADTRAYFTSATMIIAIPTGIKIFSWLATIYGGSIRL
                     ATPMLYAIAFLFLFTMGGLTGVALANASLDVAFHDMTTMLLDIFIMYYQWVTFSTYLQ
                     DTIIEVTKF"
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                     /number=1
     intron          1539. .2263
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                     /number=1
                     /cons_splice=(5'site:no, 3'site:no)
     exon            2264. .2586
                     /gene="COXI"
                     /number=2
     intron          2587. .4429
                     /gene="COXI"
                     /note="does not fit consensus"
                     /number=2
                     /cons_splice=(5'site:no, 3'site:no)
     exon            4430. .4691
                     /gene="COXI"
                     /number=3
     intron          4692. .6045
                     /gene="COXI"
                     /note="does not fit consensus"
                     /number=3
                     /cons_splice=(5'site:no, 3'site:no)
     exon            6046. .6183
                     /gene="COXI"
                     /number=4
     intron          6184. .7895
                     /gene="COXI"
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                     /number=4
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     exon            7896. .8390
                     /gene="COXI"
                     /number=5
     3'UTR           8391. .8622
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BASE COUNT     3683 a    624 c    774 g   3541 t
ORIGIN

  Query Match            10.2%;  Score 49.8;  DB 8;  Length 8622;
  Best Local Similarity  57.0%;  Pred. No. 1.1;
  Matches   90;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy    307 AACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCACGCA 366
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Db   8446 AAACTTAATATATATATAATAATATTCTTATAAAAAAAAAATATATAAAAAATATAAAAT 8505

Qy    367 GTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGTTATG 426
          |||    | | ||| || ||| ||||| | | |||||       | | |||||  |||
Db   8506 TTATTAAAATATCTTAATATATTTATATAAATAAATATTAATATAATCCTATTATATATA 8565

Qy    427 CACTTCTATCATATGGAATAAACATCAATAAGTAATTT 464
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Db   8566 TATATATATATAAAATAATATATATATAATTAATAT 8603


RESULT 14
PFMAL1P1
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LOCUS       PFMAL1P1              152409 bp    DNA     linear   HTG 11-AUG-1999
DEFINITION  Plasmodium falciparum 3D7 chromosome 1, *** SEQUENCING IN PROGRESS
            ***, in unordered pieces.
ACCESSION   AL031744
VERSION     AL031744.7  GI:5731887
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Plasmodium falciparum 3D7.
  ORGANISM  Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 152409)
  AUTHORS   Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.
            and Barrell,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,
            The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
            CB10 1SA, UK
COMMENT     On Aug 12, 1999 this sequence version replaced gi:5706481.
            For more information about this sequence or the Malaria Project,
            see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This
            sequence is unfinished and does not necessarily represent the
            correct sequence. Work on the sequence is in progress and the
            release of this data is based on the understanding that the
            sequence may change as work continues. The sequence may be
            contaminated with foreign sequence from E.coli, yeast, vector,
            phage etc.
            Order of segments is not known; 800 n's separate segments.
            * NOTE: This is a 'working draft' sequence.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
FEATURES             Location/Qualifiers
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                     /strain="3D7"
                     /db_xref="taxon:36329"
                     /chromosome="1"
BASE COUNT    52517 a  14209 c  13674 g  51206 t  20803 others
ORIGIN

  Query Match            10.1%;  Score 49.6;  DB 2;  Length 152409;
  Best Local Similarity   57.6%;  Pred. No. 0.91;
  Matches  106;  Conservative    0;  Mismatches   76;  Indels    2;  Gaps    1;

Qy     307 AACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCACGCA 366
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Qy     367 GTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGTTATG 426
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Qy     427 CACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAA 486
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RESULT 15
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LOCUS       AC005506              205429 bp    DNA     linear   HTG 12-AUG-2000
DEFINITION  Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
            PROGRESS ***, 4 unordered pieces.
ACCESSION   AC005506
VERSION     AC005506.8  GI:9797717
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Plasmodium falciparum.
  ORGANISM  Plasmodium falciparum
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1  (bases 1 to 205429)
  AUTHORS   Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T.,
            Kurdi,O.B., Conway,A.B. and Davis,R.W.
  TITLE     Plasmodium falciparum 3D7 chromosome 12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 205429)
  AUTHORS   Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
            Center, Stanford University, 855 California Avenue, Palo Alto, CA
            94304, USA
COMMENT     On Aug 12, 2000 this sequence version replaced gi:8810449.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1   132269: contig of 132269 bp in length
            *  132270   132469: gap of unknown length
            *  132470   192227: contig of 59758 bp in length
            *  192228   192427: gap of unknown length
            *  192428   203864: contig of 11437 bp in length
            *  203865   204064: gap of unknown length
            *  204065   205429: contig of 1365 bp in length.
FEATURES             Location/Qualifiers
     source          1. .205429
                     /organism="Plasmodium falciparum"
                     /db_xref="taxon:5833"
                     /chromosome="12"
                     /clone="PFYAC357"
                     /clone="3D7"
BASE COUNT    83932 a  17937 c  19766 g  83194 t    600 others
ORIGIN

  Query Match            10.1%;  Score 49.6;  DB 2;  Length 205429;
  Best Local Similarity   56.7%;  Pred. No. 0.89;
  Matches  115;  Conservative    0;  Mismatches   80;  Indels    8;  Gaps    1;

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           | |  || | || |  |   || |   |||||   |  || |    ||| || ||||  |
Db   82682 TATATAAAGAATATATTTATACTTTTTGATGTTATTATAAAAAATATTAAAAAAAAAAAA 82741

Qy     348 AATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGN 407
           || || ||||||  |   || |||      | || || ||| | | |   | |
Db   82742 AAAAATTAAAATAAAAAAAGGATACTATATAATTTATTTATTTTTTTTTTTAA------- 82794

Qy     408 GCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGT 467
             | ||  |||| |  |.||  | ||| |||| |||| | ||||| |    ||||| |
Db   82795 -TAAAATATATTTTTATTACATATATATAATATATAATACATATCAAAATAGGATTTCAT 82853

Qy     468 NTCCAAAAAAAAAAAAAAAAAAA 490
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Search completed: May  8, 2003, 06:39:41
Job time : 2168.78 secs
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GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:54:13 ; Search time 57.7389 Seconds
(without alignments)
2602.608 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507
Perfect score: 490
Sequence: 1 TGTCAAACACACACATAACA.....CAAAAAAAAAAAAAAAAAAA 490

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	488	99.6	507	3	US-08-766-355-10	Sequence 10, Appl
	3	488	99.6	507	4	US-09-003-198A-10	Sequence 10, Appl
	4	488	99.6	507	4	US-09-428-805-10	Sequence 10, Appl
	5	301.8	61.6	327	3	US-08-766-355-9	Sequence 9, Appli
	6	301.8	61.6	327	4	US-09-003-198A-9	Sequence 9, Appli
	7	301.8	61.6	327	4	US-09-428-805-9	Sequence 9, Appli
	8	234	47.8	250	3	US-08-766-355-13	Sequence 13, Appl
	9	234	47.8	250	4	US-09-003-198A-13	Sequence 13, Appl
	10	234	47.8	250	4	US-09-428-805-13	Sequence 13, Appl
	11	228.6	46.7	293	3	US-08-766-355-6	Sequence 6, Appli
	12	228.6	46.7	293	4	US-09-003-198A-6	Sequence 6, Appli
	13	228.6	46.7	293	4	US-09-428-805-6	Sequence 6, Appli
	14	181.2	37.0	189	4	US-09-003-198A-18	Sequence 18, Appl
	15	179.8	36.7	200	3	US-08-766-355-5	Sequence 5, Appli
	16	179.8	36.7	200	4	US-09-003-198A-5	Sequence 5, Appli
	17	179.8	36.7	200	4	US-09-428-805-5	Sequence 5, Appli
	18	54	11.0	62	3	US-08-766-355-11	Sequence 11, Appl
	19	54	11.0	62	4	US-09-003-198A-11	Sequence 11, Appl
	20	54	11.0	62	4	US-09-428-805-11	Sequence 11, Appl
	21	41.4	8.4	751	4	US-09-280-116-86	Sequence 86, Appl
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	23	40	8.2	141	1	US-08-777-192-35	Sequence 35, Appl
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c	25	39.6	8.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c	26	39	8.0	47	3	US-08-766-355-12	Sequence 12, Appl
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	30	37.6	7.7	946	3	US-08-916-443A-15	Sequence 15, Appl
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c	32	36.6	7.5	636	4	US-08-998-416-1137	Sequence 1137, Ap
	33	36.6	7.5	6124	4	US-08-213-419B-3	Sequence 3, Appli
	34	36.4	7.4	1872	4	US-09-291-922-27	Sequence 27, Appl
	35	35.8	7.3	1620	3	US-08-985-950-11	Sequence 11, Appl
	36	35.8	7.3	9636	1	US-08-323-170B-1	Sequence 1, Appli
	37	35.8	7.3	9636	4	US-08-954-441-1	Sequence 1, Appli
c	38	35.6	7.3	3463	4	US-09-189-462-3	Sequence 3, Appli
c	39	35.4	7.2	963	4	US-09-134-001C-1367	Sequence 1367, Ap
c	40	35.4	7.2	1364	4	US-09-428-034-1	Sequence 1, Appli
	41	35.2	7.2	1212	4	US-09-182-145-34	Sequence 34, Appl
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	43	35.2	7.2	33000	4	US-09-215-694-18	Sequence 18, Appl
c	44	35	7.1	427	4	US-09-438-906-31	Sequence 31, Appl
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ALIGNMENTS

RESULT 1
US-09-003-198A-19
; Sequence 19, Application US/09003198A
; Patent No. 6316407
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,198A
; FILING DATE: 07-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-003-198A-19

Query Match 99.6%; Score 488; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 490; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
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Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
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Qy    361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420
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Qy    481 AAAAAAAAAA 490
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Db    481 AAAAAAAAAA 490


RESULT 2
US-08-766-355-10
; Sequence 10, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  507 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 424, 485)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-10

  Query Match             99.6%;  Score 488;  DB 3;  Length 507;
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  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 137

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Db    198 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 257

Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
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Db    318 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 377

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Qy    481 AAAAAAAAAA 490
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Db    498 AAAAAAAAAA 507


RESULT 3
US-09-003-198A-10
; Sequence 10, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/003,198A
;       FILING DATE:  07-JAN-1998
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Patterson, Melinda L.
;       REGISTRATION NUMBER:  33,062
;       REFERENCE/DOCKET NUMBER:  MOBT:193
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (713) 787-1400
;       TELEFAX:  (713) 787-1440
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  507 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  modified_base
;       LOCATION:  one-of(17, 424, 485)
;       OTHER INFORMATION:  /mod_base= OTHER
;       OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-10

  Query Match             99.6%;  Score 488;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-118;
  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy      61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 137

Qy     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db     318 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 377

Qy     361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420
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Db     378 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 437

Qy     421 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 480
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Db     438 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 497

Qy     481 AAAAAAAAA 490
          |||||||||
Db     498 AAAAAAAAA 507


RESULT 4
US-09-428-805-10
; Sequence 10, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  507 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  modified_base
;       LOCATION:  one-of(17, 424, .485)
;       OTHER INFORMATION:  /mod_base= OTHER
;       OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-10

  Query Match             99.6%;  Score 488;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-118;
  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy      61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
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Db      78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 137

Qy     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db     198 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 257

Qy     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
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Db     258 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 317

Qy     301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360
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Qy    361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420
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Qy    481 AAAAAAAAA 490
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Db    498 AAAAAAAAA 507


RESULT 5
US-08-766-355-9
; Sequence 9, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-9

  Query Match             61.6%;  Score 301.8;  DB 3;  Length 327;
  Best Local Similarity   97.6%;  Pred. No. 3.7e-70;
  Matches  319;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

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Qy    225 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 284
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Db    301 TCGTNTCCAAAAAAAAAAAAAAAAAAA 327


RESULT 6
US-09-003-198A-9
; Sequence 9, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-9

  Query Match             61.6%;  Score 301.8;  DB 4;  Length 327;
  Best Local Similarity   97.6%;  Pred. No. 3.7e-70;
  Matches  319;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;
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Qy    225 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 284
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Db    241 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 300

Qy    464 TCGTNTCCAAAAAAAAAAAAAAAAAAA 490
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Db    301 TCGTNTCCAAAAAAAAAAAAAAAAAAA 327


RESULT 7
US-09-428-805-9
; Sequence 9, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-9

  Query Match             61.6%;  Score 301.8;  DB 4;  Length 327;
  Best Local Similarity   97.6%;  Pred. No. 3.7e-70;
  Matches  319;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

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Qy    225 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTTCGTTGTTAGTGTACTAAA 284
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Qy    404 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 463
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Qy    464 TCGTNTCCAAAAAAAAAAAAAAAAAAA 490
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Db    301 TCGTNTCCAAAAAAAAAAAAAAAAAAA 327


RESULT 8
US-08-766-355-13
; Sequence 13, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 base pairs
```

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;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-766-355-13

  Query Match             47.8%;  Score 234;  DB 3;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-52;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 119
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Db       9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 68

Qy     120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
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RESULT 9
US-09-003-198A-13
; Sequence 13, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-003-198A-13

  Query Match             47.8%;  Score 234;  DB 4;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-52;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 119
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Db       9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 68

Qy     120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
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Db      69 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 128

Qy     180 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 239
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Db     129 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 188

Qy     240 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 293
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Db     189 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 242


RESULT 10
US-09-428-805-13
; Sequence 13, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-428-805-13

  Query Match             47.8%;  Score 234;  DB 4;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-52;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 119
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Qy     120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
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Db      69 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 128

Qy     180 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 239
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Qy     240 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 293
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Qy    120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
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Qy    240 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 293
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RESULT 11
US-08-766-355-6
; Sequence 6, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 265)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-6

  Query Match             46.7%;  Score 228.6;  DB 3;  Length 293;
  Best Local Similarity   89.1%;  Pred. No. 4.5e-51;
  Matches  246;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
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Qy     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
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Db     78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCCTCGTTC 137

Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Qy    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
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Db    198 CATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCACTGCAAAACCAAAGAACACTTAC 257

Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
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RESULT 12
US-09-003-198A-6
; Sequence 6, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 265)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-6

  Query Match             46.7%;  Score 228.6;  DB 4;  Length 293;
  Best Local Similarity   89.1%;  Pred. No. 4.5e-51;
  Matches  246;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

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Db     18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
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Db     78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCCTCGTTC 137

Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db    138 TCTTTGTTGAACAAGAAATTATGGTGACCGAGGCAGCTACTTGTGAGAATTTGGCTAACA 197

Qy    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
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Db    198 CATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCACTGCAAAACCAAAGAACACTTAC 257

Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
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Db    258 TTAGCGGNAGGTGCAGGGACGACTTCCGCTGCTGCT 293


RESULT 13
US-09-428-805-6
; Sequence 6, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  293 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 265)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-6

  Query Match           46.7%;  Score 228.6;  DB 4;  Length 293;
  Best Local Similarity  89.1%;  Pred. No. 4.5e-51;
  Matches  246;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy      1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
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Db     18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
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Db     78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCCTCGTTC 137

Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db    138 TCTTTGTTGAACAAGAAATTATGGTGACCGAGGCAGCTACTTGTGAGAATTTGGCTAACA 197

Qy    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
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RESULT 14
US-09-003-198A-18
; Sequence 18, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  189 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-003-198A-18

  Query Match           37.0%;  Score 181.2;  DB 4;  Length 189;
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Qy    274 GGTGTA 279
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RESULT 15
US-08-766-355-5
; Sequence 5, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
; . INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  17
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-5

  Query Match             36.7%;  Score 179.8;  DB 3;  Length 200;
  Best Local Similarity   98.9%;  Pred. No. 2.2e-38;
  Matches  181;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     94 CTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 153
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Db     18 CAGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 77

Qy    154 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 213
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Db     78 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 137

Qy    214 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 273
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Qy    274 GGT 276
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SUMMARIES

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	2	488	99.6	507	9	US-10-010-731-10	Sequence 10, Appl
	3	301.8	61.6	327	9	US-10-010-731-9	Sequence 9, Appli
	4	234	47.8	250	9	US-10-010-731-13	Sequence 13, Appl
	5	228.6	46.7	293	9	US-10-010-731-6	Sequence 6, Appli
	6	181.2	37.0	189	9	US-10-010-731-18	Sequence 18, Appl
	7	179.8	36.7	200	9	US-10-010-731-5	Sequence 5, Appli
	8	127.4	26.0	494	9	US-09-805-694B-5	Sequence 5, Appli
	9	127.4	26.0	563	9	US-10-178-213-439	Sequence 439, App
	10	95.2	19.4	464	9	US-10-178-213-379	Sequence 379, App
	11	93.2	19.0	420	9	US-10-178-213-436	Sequence 436, App
	12	93	19.0	461	9	US-10-178-213-451	Sequence 451, App
	13	54	11.0	62	9	US-10-010-731-11	Sequence 11, Appl
	14	49.6	10.1	338	9	US-10-178-213-427	Sequence 427, App
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	16	44.2	9.0	438	9	US-10-178-213-418	Sequence 418, App
	17	44.2	9.0	455	9	US-10-178-213-415	Sequence 415, App
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	19	44	9.0	293	9	US-10-178-213-421	Sequence 421, App
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c	21	41.8	8.5	7544	9	US-10-239-676-5	Sequence 5, Appli
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c	23	40.6	8.3	6815	9	US-10-239-676-50	Sequence 50, Appl
c	24	40.2	8.2	8588	9	US-10-239-676-178	Sequence 178, App
c	25	40.2	8.2	17419	9	US-10-239-676-99	Sequence 99, Appl
	26	40	8.2	141	10	US-09-759-584-35	Sequence 35, Appl
c	27	40	8.2	211	10	US-09-960-352-2195	Sequence 2195, Ap
c	28	39.8	8.1	215	9	US-10-060-036-2168	Sequence 2168, Ap
c	29	39.8	8.1	8801	9	US-10-239-676-144	Sequence 144, App
c	30	39.8	8.1	9293	9	US-10-239-676-25	Sequence 25, Appl
c	31	39.8	8.1	17142	9	US-10-239-676-206	Sequence 206, App
c	32	39.6	8.1	11260	9	US-10-239-676-19	Sequence 19, Appl
c	33	39.4	8.0	479	10	US-09-960-352-12872	Sequence 12872, A
c	34	39.2	8.0	7810	9	US-10-239-676-142	Sequence 142, App
c	35	39.2	8.0	11812	9	US-10-239-676-210	Sequence 210, App
c	36	39	8.0	47	9	US-10-010-731-12	Sequence 12, Appl
c	37	39	8.0	8866	9	US-10-239-676-139	Sequence 139, App
c	38	38.4	7.8	2000	9	US-09-938-842A-2900	Sequence 2900, Ap
	39	38.4	7.8	5689	9	US-10-239-676-89	Sequence 89, Appl
c	40	38.2	7.8	9539	9	US-10-239-676-52	Sequence 52, Appl
c	41	38.2	7.8	17848	9	US-10-239-676-28	Sequence 28, Appl
c	42	38	7.8	431	10	US-09-960-352-5558	Sequence 5558, Ap
	43	38	7.8	1622	9	US-09-938-842A-4417	Sequence 4417, Ap
c	44	38	7.8	15649	9	US-10-239-676-103	Sequence 103, App
	45	37.8	7.7	236	9	US-09-991-936-1213	Sequence 1213, Ap

ALIGNMENTS

RESULT 1
US-10-010-731-19
; Sequence 19, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip Maganlal
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,731
; FILING DATE: 13-No. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/003,198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 490 base pairs

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;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

  Query Match             99.6%;  Score 488;  DB 9;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-114;
  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60

Qy     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120

Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180

Qy    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240

Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300

Qy    301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360
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Db    301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360

Qy    361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420

Qy    421 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 480

Qy    481 AAAAAAAAAA 490
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Db    481 AAAAAAAAAA 490


RESULT 2
US-10-010-731-10
; Sequence 10, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 507 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  one-of(17, 424, 485)
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

  Query Match             99.6%;  Score 488;  DB 9;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-114;
  Matches  490;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     18 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATC 77

Qy     61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 137

Qy    121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 197

Qy    181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 257

Qy    241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC 317

Qy    301 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 TCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATG 377

Qy    361 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 420
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Db    378 CACGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTA 437

Qy    421 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 GTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAA 497

Qy    481 AAAAAAAAAA 490
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Db    498 AAAAAAAAAA 507


RESULT 3
US-10-010-731-9
; Sequence 9, Application US/10010731
; Publication No: US20030041347A1
;   GENERAL INFORMATION:
```

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;       APPLICANT: Liang, Jihong
;                  Shah, Dilip Maganlal
;                  Wu, Yonnie S.
;                  Rosenberger, Cindy A.
;                  Hakimi, Salim
;       TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                           Controlling Plant Pathogenic Fungi
;       NUMBER OF SEQUENCES: 19
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Arnold White & Durkee
;            STREET: P.O. Box 4433
;            CITY: Houston
;            STATE: Texas
;            COUNTRY: USA
;            ZIP: 77210
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/010,731
;            FILING DATE: 13-No. US20030041347A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/003,198
;            FILING DATE: 07-JAN-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Patterson, Melinda L.
;            REGISTRATION NUMBER: 33,062
;            REFERENCE/DOCKET NUMBER: MOBT:193
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (713) 787-1400
;            TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 327 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       FEATURE:
;            NAME/KEY:  modified_base
;            LOCATION:  one-of(244, 305)
;            OTHER INFORMATION:  /mod_base= OTHER
;            /note= "N = A or C or G or T"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

  Query Match           61.6%;  Score 301.8;  DB 9;  Length 327;
  Best Local Similarity  97.6%;  Pred. No. 3.6e-67;
  Matches  319;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy    165 GAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 224
          |||||||||||  ||||| ||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGAATTTGGCGGATAAGTATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 60

Qy    225 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 284
          |||||||||||||||||||||||||||||||||| ||||| || || | ||||||||||
Db     61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy    285 AGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAA 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAA 180

Qy    345 CTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATG-ACTCAATA 403
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    181 CTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGTACTCAATA 240

Qy    404 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTAATT 300

Qy    464 TCGTNTCCAAAAAAAAAAAAAAAAAAA 490
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Db    301 TCGTNTCCAAAAAAAAAAAAAAAAAAA 327


RESULT 4
US-10-010-731-13
; Sequence 13, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;       APPLICANT: Liang, Jihong
;                  Shah, Dilip Maganlal
;                  Wu, Yonnie S.
;                  Rosenberger, Cindy A.
;                  Hakimi, Salim
;       TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                           Controlling Plant Pathogenic Fungi
;       NUMBER OF SEQUENCES: 19
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Arnold White & Durkee
;            STREET: P.O. Box 4433
;            CITY: Houston
;            STATE: Texas
;            COUNTRY: USA
;            ZIP: 77210
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/010,731
;            FILING DATE: 13-No. US20030041347A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/003,198
;            FILING DATE: 07-JAN-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Patterson, Melinda L.
;            REGISTRATION NUMBER: 33,062
;            REFERENCE/DOCKET NUMBER: MOBT:193
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (713) 787-1400
;            TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 250 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

  Query Match           47.8%;  Score 234;  DB 9;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-50;
  Matches  234;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTT 68

Qy    120 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 179
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Db     69 CTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGAT 128

Qy    180 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 239
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Db    129 AAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCA 188

Qy    240 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 293
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Db    189 GTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 242
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RESULT 5
US-10-010-731-6
; Sequence 6, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 293 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  one-of(17, 265)
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-010-731-6

  Query Match             46.7%;  Score 228.6;  DB 9;  Length 293;
  Best Local Similarity   89.1%;  Pred. No. 1.3e-48;
  Matches  246;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

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Qy      61 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db      78 AATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCCTCGTTC 137

Qy     121 TCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATA 180
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Db     138 TCTTTGTTGAACAAGAAATTATGGTGACCGAGGCAGCTACTTGTGAGAATTTGGCTAACA 197

Qy     181 AATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
           ||| ||||||||||||||  |||||||||||  |||||||| |||||||||  ||  |
Db     198 CATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCACTGCAAAACCAAAGAACACTTAC 257

Qy     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
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Db     258 TTAGCGGNAGGTGCAGGGACGACTTCCGCTGCTGCT 293


RESULT 6
US-10-010-731-18
; Sequence 18, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 189 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-010-731-18

  Query Match             37.0%;  Score 181.2;  DB 9;  Length 189;
  Best Local Similarity   98.4%;  Pred. No. 1.1e-36;
  Matches  183;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      94 CTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 153
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 60

Qy     154 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 120

Qy     214 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 180

Qy     274 GGTGTA 279
           | || |
Db     181 GCTGGA 186
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RESULT 7
US-10-010-731-5
; Sequence 5, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 200 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  17
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-731-5

  Query Match             36.7%;  Score 179.8;  DB 9;  Length 200;
  Best Local Similarity   98.9%;  Pred. No. 2.7e-36;
  Matches  181;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      94 CTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 153
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      18 CAGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAG 77

Qy     154 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 213
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      78 CCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACA 137

Qy     214 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 273
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 CTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCT 197

Qy     274 GGT 276
           | ||
Db     198 GCT 200
```

```
RESULT 8
US-09-805-694B-5
; Sequence 5, Application US/09805694B
; Publication No. US20030041350A1
; GENERAL INFORMATION:
;  APPLICANT: Kinney, Anthony
;  TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
;  FILE REFERENCE: BB1432 US NA
;  CURRENT APPLICATION NUMBER: US/09/805,694B
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,823
;  PRIOR FILING DATE: 2000-03-16
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
;   LENGTH: 494
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (9)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (388)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (392)..(393)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (460)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (463)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (468)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-805-694B-5

  Query Match             26.0%;  Score 127.4;  DB 9;  Length 494;
  Best Local Similarity   68.4%;  Pred. No. 8.3e-23;
  Matches  225;  Conservative    0;  Mismatches   91;  Indels   13;  Gaps    3;

Qy      46 TTATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCT 105
           ||| ||| |          ||||| || | ||||||||||||||| ||||||| || ||||
Db      17 TTACATACACGTGAATCACTAATTAAGCCATGGAGAAGAAATCAATAGCTGGGTTGTGCT 76

Qy     106 TCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACAT 162
           |||||||| | |||||||||||||| |||||| |||||||    || || || |  || |
Db      77 TCCTCTTCCTTGTTCTCTTTGTTGCTCAAGAAGTTGTGGTGCAAACTGAGGCAAAGACTT 136

Qy     163 GTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTC 216
           | |||||  |||| |||| ||| ||||| ||||||||      | |  | || ||   ||
Db     137 GCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGATGATC 196

Qy     217 ACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
           ||||||  | |||||| ||    | || || || || |||||||| || ||||| ||||
Db     197 ACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGTTGGT 256

Qy     277 GTACTAAAAGATGTTAAATGGATC----TCCTCCAACATCAAGATGTGCATGGAATAGTC 332
           | || ||||  ||||||||||||      ||||||| | |||| |      | |  |
Db     257 GCACCAAAAACTGTTAAATGGATCCATTCACTCCAACGTGAAGAAGATGCATGCAGCGCT 316

Qy     333 TTTATAATAAAACTAAATAAATAAAATGC 361
           || ||  |||| || |   |  | || |
Db     317 ATTTTATAAAAAATACAACTACTATATAC 345


RESULT 9
US-10-178-213-439
; Sequence 439, Application US/10178213
```

```
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 439
;   LENGTH: 563
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (106)...(333)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (190)...(330)
US-10-178-213-439

  Query Match             26.0%;  Score 127.4;  DB 9;  Length 563;
  Best Local Similarity   65.9%;  Pred. No. 8.8e-23;
  Matches  234;  Conservative    0;  Mismatches  111;  Indels   10;  Gaps    3;

Qy      50 ATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCT 109
           ||  ||| | | |    | | | ||||||||||||||||||||| ||||| || |||| |||
Db      81 ATTAATTAAGCTAAGGTAGCTAGCTATGGAGAAGAAATCACTGGCTGGATTCTGCTGCCT 140

Qy     110 CTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGA 166
           |||| |  |||||||| |||| |||||||| ||||||   ||||| || || ||||||||
Db     141 CTTCCTCATTCTCTTTCTTGCTCAAGAAATAGTGGTGAAAACAGAGGCAAGGACATGTGA 200

Qy     167 GAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTG 220
           || | ||||||| | ||| |||||||| || ||      | || | || ||   ||||||
Db     201 GAGTCTGGCAGACACATACAGGGGACCCTGTTTCACAGATGGTAGCTGCGATGATCACTG 260

Qy     221 CACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTAC 280
           ||  | ||||||| ||  | | |||||||| || ||  | || || ||||| ||||| ||
Db     261 CAAGAACAAAGAGCACTTAATCAGTGGAAGATGCAGAAATGATTTTCGCTGTTGGTGCAC 320

Qy     281 TAAAAGATGTTAAATGGATCTC-CTCCAACATCAAGATGTGCATGGAATAGTCTTTATAA 339
           | ||  ||||||||      |  |||  ||||||||||       ||    | |||
Db     321 CAGAAACTGTTAAATTCTGGACTTTCCCCCATCAAGATGCATGCACAACGAACCTTAATT 380

Qy     340 TAAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATAT 394
           |  || | |   | |||  ||  | ||||  || ||||   |   | | |||
Db     381 ATTATATATACATCAATAATAAACAAAATATAAATAAAACTAGCTGCCTCTGTAT 435


RESULT 10
US-10-178-213-379
; Sequence 379, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 379
;   LENGTH: 464
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (32)...(256)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (116)...(253)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2
;   OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

  Query Match             19.4%;  Score 95.2;  DB 9;  Length 464;
  Best Local Similarity   61.8%;  Pred. No. 1.2e-14;
  Matches  225;  Conservative    0;  Mismatches  123;  Indels   16;  Gaps    4;

Qy      50 ATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCT 109
           ||  ||| |   |  | |   || |||||||||||||||| | ||||| || |||| |||
Db       7 ATTAATTAAGTGAATTTAAGCAATTATGGAGAAGAAATCAGTCGCTGGTTTTTGCTGCCT 66

Qy     110 CTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGA 166
           | || | || |||||||||| || ||||| ||||||   ||||| || ||||||||||
Db      67 CCTCCTTGTCCTCTTTGTTGCTCAGGAAATAGTGGTGAAAACAGAGGCAAGAACATGTGA 126

Qy     167 GAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGACACTCACTG 220
           || |  |||||| | ||| |||||||| || || |      || | || ||   ||| ||
Db     127 GAGTCCGGCAGACACATACAGGGGACCCTGTTTCACTGAGGGTAGCTGCGATGATCATTG 186

Qy     221 CACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTAC 280
           ||  | ||||||  ||  | | |||||||  || |   |  | ||   |||||||| ||
Db     187 CAAGAACAAAGAACACTTAATCAGTGGAACATGCA---AACAGTTAGCCTGCTGGTGCAC 243

Qy     281 TAAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAAT 340
           | ||  |||||| |   |     | || || |     ||||    |  | ||| || |
Db     244 CAGAAACTGTTAATTAATT----ACTAATATTATTGGATGCAGTACAGTGCCTTAATTAA 299

Qy     341 AAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCA 400
           |     || ||||||       | |||||   | |||  ||  || |    |   | |
Db     300 TTATTACTATCAATAAATAAATTACTGTATACAAATAACAGCACTTAAACTGCTTCTTAA 359

Qy     401 ATAT 404
           |||
Db     360 TTAT 363


RESULT 11
US-10-178-213-436
; Sequence 436, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
```

```
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 436
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)...(264)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (118)...(261)
US-10-178-213-436

  Query Match             19.0%;  Score 93.2;  DB 9;  Length 420;
  Best Local Similarity   70.3%;  Pred. No. 3.7e-14;
  Matches  173;  Conservative    0;  Mismatches   58;  Indels   15;  Gaps    3;

Qy      65 TAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTC---TTCTTGGTTCT 121
           |||   || |||||||| |||||||  | ||||| || || | ||||    || | ||| |
Db      21 TAAGTGAATTATGGAGAGGAAATCAGTTGCTGGATTGTGGTGCCTCATGCTCGTTGTTGT 80

Qy     122 CTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGAGAATTTGGCAGA 178
           || |||||| ||||| | ||||||    ||||| |  |  |||||||||||| | |||||
Db      81 GTTAGTTGCAGAAGAAGTAGTGGTGAAAACAGAGGGAAAGACATGTGAGAATCTTGCAGA 140

Qy     179 TAAATATAGGGGACCATGCTTTAGTG---------GTTGTGACACTCACTGCACAACCAA 229
           || ||  ||||| ||||||||   ||         | ||  ||  ||||||||  | |||
Db     141 TACATTCAGGGGTCCATGCTTCCCTGGAACCGCCAGCTGCAACGATCACTGCAAGAACAA 200

Qy     230 AGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATG 289
           ||||  ||    | || |||||||| || ||||| || |||||||||||  || ||||  ||
Db     201 AGAGCACTTGCTCAGCGGAAGGTGCAGAGACGATTTTCGCTGCTGGTGCACCAAAAACTG 260

Qy     290 TTAAAT 295
           |||| |
Db     261 TTAATT 266


RESULT 12
US-10-178-213-451
; Sequence 451, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 451
;   LENGTH: 461
;   TYPE: DNA
;   ORGANISM: Arachis hypogaea
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (44)...(271)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (128)...(268)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
;   OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

  Query Match             19.0%;  Score 93;  DB 9;  Length 461;
  Best Local Similarity   68.5%;  Pred. No. 4.3e-14;
  Matches  161;  Conservative    0;  Mismatches   65;  Indels    9;  Gaps    2;

Qy      70 AAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTG 129
           || | |||| |  |||||| ||| | || || |||||| || || |  | ||| ||||||
Db      39 AAGCCATGGCGGGGAAATCTCTAACCGGGTTTTGCTTCATCCTCCTCCTCCTCGTTGTTG 98

Qy     130 CACAAGAAATTGTGGTGACA---GAAGCCAGAACATGTGAGAATTTGGCAGATAAATATA 186
           | || |||| ||||||  |   || ||   ||| ||||||||  |||| ||||  || |
Db      99 CTCAGGAAATGGTGGTGCAAAGTGAGGCAGCAACGTGTGAGAACCTGGCGGATACCTACA 158

Qy     187 GGGGACCATGCTTTA------GTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAG 240
           |||||||||||||| |      |  | || |||   |||||||  | ||| ||| ||
Db     159 GGGGACCATGCTTCACCACCGGAAGCTGCGACGACCACTGCAAGAACAAGGAGCACCTGC 218

Qy     241 TTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAAT 295
           | || ||  | ||  | ||||| |||||||| ||||| || | ||  ||||||||
Db     219 TCAGCGGCCGCTGCCGCGACGATTTCCGCTGTTGGTGCACCAGAAACTGTTAAAT 273


RESULT 13
US-10-010-731-11
; Sequence 11, Application US/10010731
; Publication No. US20030041347A1
;  GENERAL INFORMATION:
;       APPLICANT: Liang, Jihong
;                  Shah, Dilip Maganlal
;                  Wu, Yonnie S.
;                  Rosenberger, Cindy A.
;                  Hakimi, Salim
;       TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                           Controlling Plant Pathogenic Fungi
;       NUMBER OF SEQUENCES: 19
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Arnold White & Durkee
;            STREET: P.O. Box 4433
;            CITY: Houston
;            STATE: Texas
;            COUNTRY: USA
;            ZIP: 77210
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/010,731
;            FILING DATE: 13-No. US20030041347A1-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/003,198
;            FILING DATE: 07-JAN-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Patterson, Melinda L.
;            REGISTRATION NUMBER: 33,062
```

```
;            REFERENCE/DOCKET NUMBER: MOBT:193
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (713) 787-1400
;            TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 62 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-010-731-11

  Query Match             11.0%;  Score 54;  DB 9;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      60 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTC 113
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 CAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTC 62


RESULT 14
US-10-178-213-427
; Sequence 427, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 427
;   LENGTH: 338
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (14)...(244)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (101)...(241)
US-10-178-213-427

  Query Match             10.1%;  Score 49.6;  DB 9;  Length 338;
  Best Local Similarity   50.7%;  Pred. No. 0.0039;
  Matches  149;  Conservative    0;  Mismatches  139;  Indels    6;  Gaps    1;

Qy      75 ATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTTGCACAA 134
           |||  ||||||||||  | |||    | | |||| || || |  || |||| | | | |||
Db      20 ATGATGAAGAAATCAATTGCTTTGATCTTCTTCTTCCTCCTCCTTGTCTTCGCTTCTCAA 79

Qy     135 GAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCA 194
           | |||| ||| ||||| ||    ||  ||      |    | | | || ||| |||
Db      80 ATGGTGGTGGAGACGGAAGCGAGGGTGTGCCAGTCACAGAGCCACCACTTTAAGGGGCCA 139

Qy     195 TGCTTTAGTGGTTGTGACACTCA------CTGCACAACCAAAGAGAACGCAGTTAGTGGA 248
           |||||  | |    | ||  |        |||||  |   |||    | | | | | |
Db     140 TGCTTGGGAGACCATAACTGTGCACTCGTCTGCAGGAATGAAGCTTTCTCCGGTGGCCGC 199

Qy     249 AGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTCCTCCAA 308
           | | |   | | |   ||||| |  || |||||    |||| |   | ||  |   |
Db     200 TGCCGAGGTTTCCGCCGTCGCTGTTTTTGCACTAAGCTTTGTTGACAAGCTCATCAAGAG 259

Qy     309 CATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCA 362
           | | ||    | |  |   | ||||  | ||  |||   |  |||| |
Db     260 CCTTAATTACCATAAGAGACCCTTCTTATGTAATAATCAAAGGCAATTAATGAA 313


RESULT 15
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. US20020127687A1
; GENERAL INFORMATION:
;  APPLICANT: SHIGENOBU, SHUJI
;  APPLICANT:  WATANABE, HIDEMI
;  APPLICANT:  HATTORI, MASAHIRA
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
;  FILE REFERENCE: 081356/0159
;  CURRENT APPLICATION NUMBER: US/09/790,988
;  CURRENT FILING DATE:  2001-02-23
;  PRIOR APPLICATION NUMBER: JP2000-107160
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 640681
;   TYPE: DNA
;   ORGANISM: Buchnera sp.
US-09-790-988-1

  Query Match             9.1%;  Score 44.4;  DB 10;  Length 640681;
  Best Local Similarity   50.5%;  Pred. No. 3;
  Matches  105;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy     281 TAAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAAT 340
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Db  379611 TAAAAAATATGTAAAAAATAATATTCAAAATCAAGAAGTTACGCAATCTCAATTAATAAA 379552

Qy     341 AAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATATGACTCA 400
           | |   || |||  ||||| |   | | ||| || ||     | | | ||||  |
Db  379551 GAGAACTAAAAAAAGAAATGTATTTATTTTAGATAAAAAAAATTTTCTTTATAAAAGAAC 379492

Qy     401 ATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCAATAAGTA 460
           || |     | ||  ||  |   ||  |  |     |      || ||| ||   |||  |
Db  379491 ATGTAATAGAAAAAATAAAATACATCAATCTAGTGCGCCAATAACAAAAATTTCTAAACA 379432

Qy     461 ATTTCGTNTCCAAAAAAAAAAAAAAAA 488
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Db  379431 ATCAGATTTAAATAAAAAAGAAAAAGAA 379404


Search completed: May  8, 2003, 07:21:31
Job time : 292.513 secs
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GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:40:33 ; Search time 1778.2 Seconds
(without alignments)
4462.820 Million cell updates/sec

Title: US-10-010-731-10_COPY_18_507
Perfect score: 490
Sequence: 1 TGTCAAACACACACATAACA.....CAAAAAAAAAAAAAAAAAA 490

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	259.2	52.9	446	9	AJ498901	AJ498901 AJ498901
	2	156.8	32.0	574	14	BQ151477	BQ151477 NF088A06L
	3	141.4	28.9	503	12	BF633403	BF633403 NF047E03D
	4	135.2	27.6	517	9	AJ308155	AJ308155 AJ308155
	5	125.8	25.7	487	13	BI321179	BI321179 saf48d10.
c	6	115	23.5	426	12	BG838678	BG838678 Gc01_03f0
	7	106.6	21.8	438	13	BI642738	BI642738 TZS1161 T
	8	61.4	12.5	238	13	BI642792	BI642792 TZS1220 T
	9	58.2	11.9	366	13	BI321308	BI321308 saf50c11.
	10	51.8	10.6	1101	17	CNS00EVL	AL069706 Drosophil
	11	49.4	10.1	366	9	AJ503961	AJ503961 AJ503961
	12	49.4	10.1	543	12	BG453394	BG453394 NF090E11L
	13	49.2	10.0	452	12	BG452703	BG452703 NF079E01L
	14	49.2	10.0	466	14	BQ157500	BQ157500 NF105E08I
	15	49	10.0	447	13	BI269947	BI269947 NF017G12I
	16	49	10.0	450	12	BG450155	BG450155 NF014H03D
c	17	48.2	9.8	987	17	CNS014PQ	AL104456 Drosophil
c	18	47.6	9.7	406	9	AI610283	AI610283 tp14f11.x
	19	47.6	9.7	1001	17	CNS0155H	AL105023 Drosophil
c	20	47.4	9.7	1190	17	CNS02ON7	AL206908 Tetraodon
c	21	46.8	9.6	1101	17	CNS0039G	AL063921 Drosophil
	22	46.4	9.5	734	17	CNS010MP	AL099163 Drosophil
c	23	46.4	9.5	1125	9	AL547503	AL547503 AL547503
c	24	46	9.4	576	14	BQ183147	BQ183147 UI-H-EU0-
c	25	46	9.4	976	17	CNS04E5M	AL286627 Tetraodon
c	26	46	9.4	1043	17	CNS0145P	AL103735 Drosophil
	27	46	9.4	1135	17	CNS033GQ	AL226115 Tetraodon
	28	45.8	9.3	748	13	BM166819	BM166819 EST569342
c	29	45.8	9.3	937	17	CNS006ST	AL065880 Drosophil
	30	45.8	9.3	1101	17	CNS00ZBM	AL097468 Drosophil
c	31	45.4	9.3	419	17	CNS0123S	AL101074 Drosophil
	32	45.4	9.3	767	17	CNS00AQX	AL055924 Drosophil
c	33	45.4	9.3	1101	17	CNS00ZAL	AL097431 Drosophil
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	35	45.2	9.2	555	13	BM273461	BM273461 PfESToaa5
	36	45.2	9.2	558	13	BM276185	BM276185 PfESToaa7
	37	45.2	9.2	567	13	BM273583	BM273583 PfESToaa5
	38	45.2	9.2	576	13	BM274862	BM274862 PfESToaa7
c	39	45.2	9.2	1101	17	CNS001FB	AL060732 Drosophil
	40	45	9.2	759	17	CNS06QXV	AL411257 T7 end of
c	41	45	9.2	782	10	BB622182	BB622182 BB622182
c	42	44.8	9.1	386	13	BI670555	BI670555 PfESToaa0
	43	44.8	9.1	965	10	BE488181	BE488181 A9/800 Am
	44	44.8	9.1	996	17	CNS00FUH	AL071063 Drosophil
	45	44.8	9.1	1101	17	CNS017KB	AL108149 Drosophil

ALIGNMENTS

RESULT 1
AJ498901
LOCUS AJ498901 446 bp mRNA linear EST 09-AUG-2002
DEFINITION AJ498901 MTPOSE Medicago truncatula cDNA clone mt--acc955209h10, mRNA sequence.
ACCESSION AJ498901
VERSION AJ498901.1 GI:22089344
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 446)
AUTHORS Firnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T., Linke,B., Puehler,A. and Kuester,H.
TITLE Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17
JOURNAL Unpublished (2002)
COMMENT Contact: Kuester H
Lehrstuhl fuer Genetik
Universitaet Bielefeld
Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES Location/Qualifiers
source 1. .446
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="mt--acc955209h10"

/clone_lib="MTPOSE"
/tissue_type="pods including seeds"
/dev_stage="different stages of development"
/note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI; genotype A17; cDNA was prepared from polyA+ enriched RNA from developing pods including seeds harvested at different stages of development. The cDNA was directionally ligated by MediGenomix into the pGEM-T vector from Promega using GCATGCGGCCGAGGCGGCCGACATG and CTGCAGGCCATTATGGCCGGG adapters. Plasmids containing cDNA inserts were propagated in E. coli DH10B cells."
BASE COUNT 147 a 84 c 83 g 132 t
ORIGIN

Query Match 52.9%; Score 259.2; DB 9; Length 446;
Best Local Similarity 82.3%; Pred. No. 4.7e-36;
Matches 339; Conservative 0; Mismatches 55; Indels 18; Gaps 3;

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Qy      63 TCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTC 122
           | | |  || ||||||||||||||| ||||||| |||||||||||||||||| | || |||
Db      49 TATCACTAAGCTATGGAGAAGAAAACACTAGCAGGCTTATGCTTCCTCTTCCTCGTCCTC 108

Qy     123 TTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAA 182
           ||||||||||||||||||||||||| ||||| |  || ||||||||||||| ||||||
Db     109 TTTGTTGCACAAGAAATTGTGGTGACTGAAGCTAAGACTTGTGAGAATTTGGCTGATAAA 168

Qy     183 TATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTT 242
           || |||||||||||||||||||||||| |||||||||| |||||||||| ||||||
Db     169 TACAGGGGACCATGCTTTAGTGGTTGTGATACTCACTGCACTACCAAAGAGAATGCAGTT 228

Qy     243 AGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATCTC 302
           || || ||||| ||||| ||||| || || |||||||||||||  |||||||||||| |
Db     229 AGCGGCAGGTGCAGGGATGACTTTCGTTGTTGGTGTACTAAAAACTGTTAAATGGATTTT 288

Qy     303 CTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGCA 362
           |||||||| |||||  |||||| ||||  |||||||||| ||||||||||||||||||||
Db     289 CTCCAACACCAAGA--TGCATGAAATACACTTTATAATATAACTAAATAAATAAAATGCG 346

Qy     363 CGCAGTATAGCTACAACTTCATCTATATATATGACTCAATATCGNGCATAACGTATTAGT 422
           | |||              || ||| | ||      ||||||| ||||||||||||||||
Db     347 TCGATTAT------------ATATATGTGTACTCAATAATATCGTGCATAACGTATTAGT 394

Qy     423 TATGCACT----TCTATCATATGGAATAAACATCAATAAGTAATTTCGTNTC 470
           ||||||||    |||||||||||||||||| ||||||| |||||||||| ||
Db     395 TATGCACTTCTATCTATCATATGAAATAATCATCAATCAGTAATTTCGTTTC 446
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RESULT 2
BQ151477
LOCUS BQ151477 574 bp mRNA linear EST 24-APR-2002
DEFINITION NF088A06LF1F1038 Developing leaf Medicago truncatula cDNA clone NF088A06LF 5', mRNA sequence.
ACCESSION BQ151477
VERSION BQ151477.1 GI:20288536
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 574)
AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 574 Std Error: 0.00
Plate: 088 row: A column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES Location/Qualifiers
source 1..574
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF088A06LF"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."
BASE COUNT 198 a 104 c 104 g 167 t 1 others
ORIGIN

Query Match 32.0%; Score 156.8; DB 14; Length 574;
Best Local Similarity 65.2%; Pred. No. 3e-18;
Matches 304; Conservative 0; Mismatches 134; Indels 28; Gaps 4;

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Qy      50 ATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCT 109
           || ||  | ||| | | || || | ||||||||||||||| ||||||||| ||||| ||
Db      34 ATTTAAACTTCACTATCATTAAGCGATGGAGAAGAAATCAATAGCTGGCTTGTGCTTACT 93

Qy     110 CTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGAA 169
           |||| | |||||||||||||||||||||||| |||||| ||||| || || |||||| |
Db      94 CTTCCTCGTTCTCTTTGTTGCACAAGAAATTGCGGTGACTGAAGCAAGGACTTGTGAGCA 153

Qy     170 TTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGACACTCACTGCAC 223
           |||||| |||| ||| || |||||||||| |      || | |||||    |||||||
Db     154 TTTGGCTGATACATACAGAGGACCATGCTTCACGGAAGGTAGCTGTGATGACCACTGCAA 213

Qy     224 AACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAA 283
           | |||||   ||  | ||||||| | ||   |  |  |||| |  || |  || ||| |
Db     214 GAACAAAGCACACTTAATTAGTGGCACGT---GCCATAACTTTCAATGTTTCTGCACTCA 270

Qy     284 AAGATGTTAAATG----------GATCTCCTCCAACATCAAGATGTGCATGGAATAGTC 332
           ||  |||||| ||              | |||||||| |||||||
Db     271 AAACTGTTAAGTGTGGATGATGGATTAATTCTCCAACACCAAGATGCATGGAAGGACACA 330

Qy     333 TTTATAATAA--------AACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCAT 384
           | ||||  ||         |  | |||||||||     |    |  ||  |     || |
Db     331 TATATATGAATTAGACTTTATGATATAAATAAATAATAACATGCCTAAGTTGTCTTTGAA 390

Qy     385 CTATATATATGACTCAATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAA 444
           ||  ||| ||  |    |||| ||||||||| |||||||||| |  |||   ||| ||
Db     391 ATAAGTATGTGTGTACTCATCGTGCATAACGTGTTAGTTATGCATTATTATGGAATGAAA 450

Qy     445 TAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
           ||||||| |||   | |||   | |  ||||||||||||||||||
Db     451 TAAACATAAATCTATGATTATCTCTTAAAAAAAAAAAAAAAAAAAA 496
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RESULT 3
BF633403
LOCUS BF633403 503 bp mRNA linear EST 19-DEC-2000
DEFINITION NF047E03DT1F1022 Drought Medicago truncatula cDNA clone NF047E03DT 5', mRNA sequence.
ACCESSION BF633403
VERSION BF633403.1 GI:11897561
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 503)
AUTHORS Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library

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  JOURNAL   Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 503   Std Error: 0.00
            Plate: 047  row: E  column: 03
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3880"
                     /clone="NF047E03DT"
                     /clone_lib="Drought"
                     /tissue_type="Plantlets"
                     /dev_stage="Pooled timepoints"
                     /note="Vector: Lambda Zap; Contains a mixture of entire
                     plantlets harvested in a series of days-post-watering
                     timepoints. "
BASE COUNT      181 a     82 c     93 g    147 t
ORIGIN

  Query Match           28.9%;  Score 141.4;  DB 12;  Length 503;
  Best Local Similarity   64.5%;  Pred. No. 1.6e-15;
  Matches  301;  Conservative    0;  Mismatches  138;  Indels   28;  Gaps    5;

Qy      50 ATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGC-TTATGCTTCC 108
           || ||  | ||| | | || || | ||||||||||||||| |||||||| || ||||| |
Db      39 ATTTAAACTTCACTATCATTAAGCGATGGAGAAGAAATCAATAGCTGGCGTTGTGCTTAC 98

Qy     109 TCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGAGA 168
           |||||| | ||||||||||||||||||||||||| || ||| ||||| || || ||||||
Db      99 TCTTCCTCGTTCTCTTTGTTGCACAAGAAATTGCGGGGACTGAAGCAAGGACTTGTGAGC 158

Qy     169 ATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGACACTCACTGCA 222
           ||||||| |||| ||| || |||||||||| |      || | |||||    |||||||
Db     159 ATTTGGCTGATACATACAGAGGACCATGCTTCACGGAAGGTAGCTGTGATGACCACTGCA 218

Qy     223 CAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTA 282
             | |||||   ||  | |||||||  |      |  |  |||| |  || |  || |||
Db     219 AGAACAAAGCACACTTAATTAGTGGCA--CCGTGCCATAACTTTCAATGTTTCTGCACTC 276

Qy     283 AAAGATGTTAAATG-----------GATCTCCTCCAACATCAAGATGTGCATGGAATAGT 331
           |||  |||||| ||              | ||||||| |||||||
Db     277 AAAACTGTTAAGTGTGGATGATGGATTAATTCTCCAACACCAAGATGCATGGAAGGACAC 336

Qy     332 CTTTATAATAA--------AACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCA 383
             | ||||  ||         |  | |||||||||    |    |  ||  |    || |
Db     337 ATATATATGAATTAGACTTTATGATATAAATAAATAATAACATGCCTAAGTTGTCTTTGA 396

Qy     384 TCTATATATATGACTCAATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGA 443
             ||  ||| ||  |    |||| ||||||||| |||||||||| |  |||   ||| |
Db     397 AATAAGTATGTGTGTACTCATCGTGCATAACGTGTTAGTTATGCATTATTATGGAATGAA 456

Qy     444 ATAAACATCAATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
           |||||||| |||   | |||   | |  ||||||||||||||||||
Db     457 ATAAACATAAATCTATGATTATCTCTTAAAAAAAAAAAAAAAAAAAA 503


RESULT 4
AJ308155
LOCUS       AJ308155                517 bp    mRNA    linear   EST 29-OCT-2001
DEFINITION  AJ308155 SSH Pisum sativum cDNA clone PsSSH1clone91, mRNA sequence.
ACCESSION   AJ308155
VERSION     AJ308155.1  GI:16507870
KEYWORDS    EST.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Grunwald,U., Lapopin,L., Becker,A., Mann,P., Bomanskie,N.,
            Gianinazzi-Pearson,V. and Franken,P.
  TITLE     Screening for genes activated in Pisum sativum mycorrhiza by
            arbuscule development-related expression profiling
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Franken P
            Biochemistry
            Max-Planck-Institute for Terrestrial Microbiology
            Marburg, Karl-von-Frisch-Strasse, D-35043, Germany.
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Pisum sativum"
                     /cultivar="Finale"
                     /db_xref="taxon:3888"
                     /clone="PsSSH1clone91"
                     /clone_lib="SSH"
                     /tissue_type="arbuscular mycorrhiza"
                     /note="minus inoculated late mutant"
BASE COUNT      161 a     87 c    102 g    167 t
ORIGIN

  Query Match           27.6%;  Score 135.2;  DB 9;  Length 517;
  Best Local Similarity   66.1%;  Pred. No. 1.9e-14;
  Matches  213;  Conservative    0;  Mismatches  103;  Indels    6;  Gaps    1;

Qy      47 TATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTT 106
           | ||||||||||||    ||| | || | ||||| |||||| || |||||| ||| | |||
Db      50 TTTATATATTCATACCACTACTTAAGCCATGGAAAAGAAAGCAGTAGCTGCCTTGTCCTT 109

Qy     107 CCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAAGCCAGAACATGTGA 166
           ||||||  | ||||||||||||||||||| |||| | |||||  || || | ||| |||||
Db     110 CCTCTTTCTCGTTCTCTTTGTTGCACAAAAAATAGCGGTGAGTGAGGCAAAAACTTGTGA 169

Qy     167 GAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTCACTG 220
           |||||||   |  | ||  | |||||||||| |      | ||   ||  ||| || ||
Db     170 GAATTTGTTTGGCACATTCAAGGGACCATGCATCCCAGATGGTAACTGCAACAAACATTG 229

Qy     221 CACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTAC 280
           ||  | ||| ||| ||  | | ||||| ||||| ||||| || || ||||||||||| ||
Db     230 CAGGAACAACGAGCACTTACTCAGTGGGAGGTGCAGGGATGATTTTCGCTGCTGGTGCAC 289

Qy     281 TAAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAAT 340
           |  ||  |||||| |   | |  |||||||   ||           ||    |  |||
Db     290 TCGAAACTGTTAACTCAGTTTTTTCCAACACGCAGGGACATTATATGTATAAATATAAAT 349

Qy     341 AAAACTAAATAAATAAAATGCA 362
           |||||||    |  || | | |
Db     350 AAAACTATGATATGAATAAGTA 371


RESULT 5
BI321179
LOCUS       BI321179                487 bp    mRNA    linear   EST 29-NOV-2001
DEFINITION  saf48d10.y3 Gm-c1077 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1077-1723 5' similar to SW:10KD_VIGUN P18646 10 KD PROTEIN
            PRECURSOR ;, mRNA sequence.
ACCESSION   BI321179
VERSION     BI321179.1  GI:15000365
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 487)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
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          ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
          ,R., Waterston,R. and Wilson,R.
  TITLE   Public Soybean EST Project
  JOURNAL Unpublished (1999)
COMMENT   Contact: Shoemaker R/Public Soybean EST Project
          Public Soybean EST Project
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          Putative full length read
          vector to vector length is This clone is available through: ResGen,
          Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
          For further information call: (800)-533-4363 or contact via email:
          ccu@resgen.com
          Seq primer: -40RP from Gibco
          High quality sequence stop: 432.
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1077-1723"
                     /clone_lib="Gm-c1077"
                     /tissue_type="18 day old 'Williams' seedlings"
                     /dev_stage="18 day old 'Williams' seedlings"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from cotyledons of 18-day-old
                     'Williams' seedlings which were greenhouse grown in
                     potting soil. The cotyledons were flash- frozen in liquid
                     nitrogen. Stratagene's cDNA Synthesis Kit (catalog number
                     200401) was used to synthesize the cDNA. First-strand
                     synthesis was performed with 5-methyl dCTP, hence the
                     ligated cDNA was hemimethylated. A modification of
                     Stratagene's first-strand synthesis primer was used. An
                     'anchor' nucleotide (V=A, C, or G) was added to the 3' end
                     of the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
                     anchor the primer at the 5' end of the poly(A) tract.
                     After second-strand synthesis, the cDNA ends were filled
                     in with cloned Pfu DNA, ligated to EcoRI adapters and
                     subsequently phosphorylated. The cDNA was then
                     precipitated and redissolved in sterile, RNase-,
                     DNase-free water. The XhoI site within the first- strand
                     synthesis primer was then restricted by digestion with
                     XhoI from Promega (40U/ul); all XhoI sites in the cDNA
                     would be protected by their hemimethylated status. The
                     cDNA constructs were size-fractionated with  a 500bp
                     cutoff, using Sephacryl S-500 High Resolution (Pharmacia
                     Biotech) in a 2-mm diameter column and a bed volume of
                     approximately 1ml. The column eluent was precipitated,
                     redissolved, and ligated into Stratagene's pBluescript II
                     XR Predigested vector (pBluescript II SK(+) vector that
                     has been digested with EcoRI and XhoI, and phosphorylated
                     by Stratagene). This library was constucted in the
                     laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at
                     Northern Arizona University."
BASE COUNT      152 a     96 c    102 g    137 t
ORIGIN

  Query Match             25.7%;  Score 125.8;  DB 13;  Length 487;
  Best Local Similarity   68.1%;  Pred. No. 8.5e-13;
  Matches  224;  Conservative    0;  Mismatches   92;  Indels   13;  Gaps    3;

Qy      46 TTATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCT 105
           ||| ||| |         ||||| || | ||||||||||||||| ||||||| || ||||
Db      39 TTACATACACGTGAATCACTAATTAAGCCATGGAGAAGAAATCAATAGCTGGGTTGTGCT 98

Qy     106 TCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACAT 162
           |||||||| | |||||||||||||| |||||| ||||||||   || || || |  || |
Db      99 TCCTCTTCCTTGTTCTCTTTGTTGCTCAAGAAGTTGTGGTGCAAACTGAGGCAAAGACTT 158

Qy     163 GTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGACACTC 216
           | |||||  |||| |||| ||| ||||| |||||||      | |  | || ||   |
Db     159 GCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGATGATT 218

Qy     217 ACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 276
           |||||  | ||||||| ||    | || || || || |||||||| || ||||| ||||
Db     219 TCTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGTTGGT 278

Qy     277 GTACTAAAAGATGTTAAATGGATC----TCCTCCAACATCAAGATGTGCATGGAATAGTC 332
           | || ||||  |||||||||||||      ||||||| | |||| |      | |  |
Db     279 GCACCAAAAACTGTTAAATGGATCCATTCACTCCAACGTGAAGAAGATGCATGCAGCGCT 338

Qy     333 TTTATAATAAAACTAAATAAATAAAATGC 361
           || ||  |||| ||||   |  | || |
Db     339 ATTTTATAAAAAATAAAACTACTATATAC 367


RESULT 6
BG838678/c
LOCUS       BG838678               426 bp    mRNA    linear   EST 25-MAY-2001
DEFINITION  Gc01_03f01_A Gc01_AAFC_ECORC_cold_stressed_Glycine_clandestina
            Glycine clandestina cDNA clone Gc01_03f01, mRNA sequence.
ACCESSION   BG838678
VERSION     BG838678.1  GI:14204985
KEYWORDS    EST.
SOURCE      Glycine clandestina.
  ORGANISM  Glycine clandestina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris
            ,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker
            ,N.A.
  TITLE     Expressed Sequence Tags from Cold-Stressed Glycine clandestina
            Seedlings
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@em.agr.ca.
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Glycine clandestina"
                     /cultivar="1035"
                     /db_xref="taxon:45687"
                     /clone="Gc01_03f01"
                     /clone_lib="Gc01_AAFC_ECORC_cold_stressed_Glycine_clandest
                     ina"
                     /tissue_type="Leaves, stem"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Plants incubated at 2 degrees under 12 hours
                     of light/day.  Harvested  after only 2-3 days of cold
                     treatment. cDNA was prepared with the  Uni-Zap cDNA kit
                     from Stratagene.  Eco RI adapters were linked followed  by
                     digest with Xho I/Eco RI and ligated to pBluescript."
BASE COUNT      116 a     92 c     86 g    125 t      7 others
ORIGIN

  Query Match             23.5%;  Score 115;  DB 12;  Length 426;
  Best Local Similarity   71.7%;  Pred. No. 7e-11;
  Matches  177;  Conservative    4;  Mismatches   57;  Indels    9;  Gaps    2;

Qy      58 ATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGG 117
           ||  || | |   | | |||||||||||||||||| ||||| || ||||||||||| | |
Db     420 ATATATATCACTGAGCCATGGAGAAGAAATCACTTGCTGGATTGTGCTTCCTCTTCCTCG 361

Qy     118 TTCTCTTTGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGAGAATTTGG 174
           ||||||||||||||||||| ||||||||   || || || |  || || |||||  |||
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Db    360 TTCTCTTTGTTGCACAAGAATTTGTGGTGAAAACTGAGGCAAACACTTGCGAGAACCTGG 301

Qy    175 CAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGACACTCACTGCACAACCA 228
          |  ||| ||| ||||| |||||||| |      |  | || ||   ||||||||  |  |
Db    300 CTAATACATACAGGGGYCCATGCTTCACTACCGGCAGCTGCGATGATCACTGCAAGAATA 241

Qy    229 AAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGAT 288
          ||||  ||  | | || || ||||| ||||||:|:|| |||||:|||:| || | ||  |
Db    240 AAGAACACTTACTCAGCGGCAGGTGCAGGGACVAYTTTCGCTGHTGGHGCACCAGAAACT 181

Qy    289 GTTAAAT 295
          ||||| |
Db    180 GTTAATT 174


RESULT 7
BI642738
LOCUS       BI642738                438 bp    mRNA    linear   EST 10-SEP-2001
DEFINITION  TZS1161 TZS (Sapwood-heartwood transition zone of black locust -
            Summer) Robinia pseudoacacia cDNA, mRNA sequence.
ACCESSION   BI642738
VERSION     BI642738.1  GI:15544948
KEYWORDS    EST.
SOURCE      Robinia pseudoacacia.
  ORGANISM  Robinia pseudoacacia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae;
            Robinia.
REFERENCE   1  (bases 1 to 438)
  AUTHORS   Han,K.-H., Yang,J., Park,S., Paule,C.R., Kapur,V., Retzel,E.F.,
            Kamdem,D.P. and Keathley,D.E.
  TITLE     Analysis of gene expression patterns in trunk wood of a mature
            black locust (Robinia pseudoacacia)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kyung-Hwan Han
            Department of Forestry
            Michigan State University
            126 Natural Resources, East Lansing, MI 48824-1222, USA
            Tel: 517 353 4751
            Fax: 517 432 1143
            Email: hanky@msu.edu.
FEATURES             Location/Qualifiers
     source          1. .438
                     /organism="Robinia pseudoacacia"
                     /db_xref="taxon:35938"
                     /clone_lib="TZS (Sapwood-heartwood transition zone of
                     black locust - Summer)"
                     /tissue_type="sapwood-heartwood transition zone"
                     /dev_stage="mature tree"
                     /note="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi
                     IB; The cDNA library was made from the sapwood-heartwood
                     transition zone of a mature black locust tree collected in
                     Michigan in late July."
BASE COUNT      134 a     80 c     86 g    124 t     14 others
ORIGIN

  Query Match             21.8%;  Score 106.6;  DB 13;  Length 438;
  Best Local Similarity   61.8%;  Pred. No. 2e-09;
  Matches  235;  Conservative    0;  Mismatches  131;  Indels   14;  Gaps    4;

Qy     65 TAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTT 124
          |||   | | |||||||||||||||| | ||||| || |||||||||||| |  |||||||
Db     29 TAACATAGCCATGGAGAAGAAATCAGTTGCTGGATTGTGCTTCCTCTTCCTTATTCTCTT 88

Qy    125 TGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGAGAATTTGGCAGATAA 181
          |||||| |||||||| ||||||   || || ||    || ||||||||  |||| | ||
Db     89 TGTTGCTCAAGAAATAGTGGTGCAAACTGAGGCAGCGACTTGTGAGAACCTGGCTGCTAC 148

Qy    182 ATATAGGGGACCATG------CTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAA 235
          ||  ||||| | |||      || |  |   || |||  ||||||||    |    | |
Db    149 ATTCAGGGGTCTATGCATCACCTCTGCTACCTGCGACGATCACTGCAAGNTCNNNNA-CA 207

Qy    236 CGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAAAT 295
          |  | | ||||| ||||| || |||||  | ||||   |||| || ||||  ||||||||
Db    208 CTTACTCAGTGGCAGGTGCAGAGACGATGTTCGCTNGGGGTGCACCAAAAACTGTTAAAT 267

Qy    296 GGATCTCCTCCAACATCAAGATGTGCATGGAATAGTCTTTATAATAAAACTAAATAAATA 355
          |||  | |||||  || ||||||       || |        ||   | |||||||  |
Db    268 GGACTTTCTCCATAATGAAGATGCAGTGACAAAAAATAAATAAAACTATATAAATAAGTG 327

Qy    356 AAATGCACGCAGTATAGCTACAACTTCATC----TATATATATGACTCAATATCGNGCAT 411
           ||  |      |||| |  |   |  ||       |  || |  |  |    | ||||
Db    328 TAAATCTGCATCTATATATGTATTATTGTCATCTCTGAACTACGTGTGTACTGTGTGCAT 387

Qy    412 AACGTATTAGTTATGCACTT 431
          |||  | ||||||||| ||||
Db    388 AACAGACTAGTTATGTACTT 407


RESULT 8
BI642792
LOCUS       BI642792                238 bp    mRNA    linear   EST 10-SEP-2001
DEFINITION  TZS1220 TZS (Sapwood-heartwood transition zone of black locust -
            Summer) Robinia pseudoacacia cDNA, mRNA sequence.
ACCESSION   BI642792
VERSION     BI642792.1  GI:15545002
KEYWORDS    EST.
SOURCE      Robinia pseudoacacia.
  ORGANISM  Robinia pseudoacacia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae;
            Robinia.
REFERENCE   1  (bases 1 to 238)
  AUTHORS   Han,K.-H., Yang,J., Park,S., Paule,C.R., Kapur,V., Retzel,E.F.,
            Kamdem,D.P. and Keathley,D.E.
  TITLE     Analysis of gene expression patterns in trunk wood of a mature
            black locust (Robinia pseudoacacia)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kyung-Hwan Han
            Department of Forestry
            Michigan State University
            126 Natural Resources, East Lansing, MI 48824-1222, USA
            Tel: 517 353 4751
            Fax: 517 432 1143
            Email: hanky@msu.edu.
FEATURES             Location/Qualifiers
     source          1. .238
                     /organism="Robinia pseudoacacia"
                     /db_xref="taxon:35938"
                     /clone_lib="TZS (Sapwood-heartwood transition zone of
                     black locust - Summer)"
                     /tissue_type="sapwood-heartwood transition zone"
                     /dev_stage="mature tree"
                     /note="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi
                     IB; The cDNA library was made from the sapwood-heartwood
                     transition zone of a mature black locust tree collected in
                     Michigan in late July."
BASE COUNT       63 a     60 c     49 g     60 t      6 others
ORIGIN

  Query Match             12.5%;  Score 61.4;  DB 13;  Length 238;
  Best Local Similarity   68.3%;  Pred. No. 0.22;
  Matches   99;  Conservative    0;  Mismatches   43;  Indels    3;  Gaps    1;

Qy     65 TAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTT 124
          |||   | | ||||||||||||||   | ||||| || ||||||||||| |  |||||||
Db     38 TAACATAGCCATGGAGAAGAAATNNGTGGCTGGATTGTGCTTCCTCTTCCTTATTCTCTT 97

Qy    125 TGTTGCACAAGAAATTGTGGTG---ACAGAAGCCAGAACATGTGAGAATTTGGCAGATAA 181
          || ||| ||| |||| | || |   || || ||    || || || ||  |||| | ||
Db     98 TGCTGCTCAAAAAATAGCGGGGCAAACTGAGGCATCGACTTGCGAAAACCTGGCTGCTAC 157

Qy    182 ATATAGGGGACCATGCTTTAGTGGT 206
          ||  ||||| | |||| | |   ||
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Db    158 ATTCAGGGGTCTATGCATCACCTGT 182


RESULT 9
BI321308
LOCUS       BI321308                366 bp    mRNA    linear   EST 29-NOV-2001
DEFINITION  saf50c11.y3 Gm-c1077 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1077-2037 5' similar to SW:10KD_VIGUN P18646 10 KD PROTEIN
            PRECURSOR ;, mRNA sequence.
ACCESSION   BI321308
VERSION     BI321308.1  GI:15000494
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 343.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1077-2037"
                     /clone_lib="Gm-c1077"
                     /tissue_type="18 day old 'Williams' seedlings"
                     /dev_stage="18 day old 'Williams' seedlings"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from cotyledons of 18-day-old
                     'Williams' seedlings which were greenhouse grown in
                     potting soil. The cotyledons were flash- frozen in liquid
                     nitrogen. Stratagene's cDNA Synthesis Kit (catalog number
                     200401) was used to synthesize the cDNA. First-strand
                     synthesis was performed with 5-methyl dCTP, hence the
                     ligated cDNA was hemimethylated. A modification of
                     Stratagene's first-strand synthesis primer was used. An
                     'anchor' nucleotide (V=A, C, or G) was added to the 3' end
                     of the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to
                     anchor the primer at the 5' end of the poly(A) tract.
                     After second-strand synthesis, the cDNA ends were filled
                     in with cloned Pfu DNA, ligated to EcoRI adapters and
                     subsequently phosphorylated. The cDNA was then
                     precipitated and redissolved in sterile, RNase-,
                     DNase-free water. The XhoI site within the first- strand
                     synthesis primer was then restricted by digestion with
                     XhoI from Promega (40U/ul); all XhoI sites in the cDNA
                     would be protected by their hemimethylated status. The
                     cDNA constructs were size-fractionated with  a 500bp
                     cutoff, using Sephacryl S-500 High Resolution (Pharmacia
                     Biotech) in a 2-mm diameter column and a bed volume of
                     approximately 1ml. The column eluent was precipitated,
                     redissolved, and ligated into Stratagene's pBluescript II
                     XR Predigested vector (pBluescript II SK(+) vector that
                     has been digested with EcoRI and XhoI, and phosphorylated
                     by Stratagene). This library was constucted in the
                     laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at
                     Northern Arizona University."
BASE COUNT      124 a     60 c     70 g    112 t
ORIGIN

  Query Match             11.9%;  Score 58.2;  DB 13;  Length 366;
  Best Local Similarity   64.6%;  Pred. No. 0.62;
  Matches  104;  Conservative    0;  Mismatches   53;  Indels    4;  Gaps    1;

Qy    205 GTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACT 264
          | || ||   ||||||||  | ||||||| ||    | || || || || ||||||||  |
Db      3 GCTGCGATGATCACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATT 62

Qy    265 TCCGCTGCTGGTGTACTAAAAGATGTTAAATGGATC----TCCTCCAACATCAAGATGTG 320
          | ||||| ||||| || ||||  ||||||||||||      ||||||| | |||| |
Db     63 TTCGCTGTTGGTGCACCAAAAACTGTTAAATGGATCCATTCACTCCAACGTGAAGAAGAT 122

Qy    321 CATGGAATAGTCTTTATAATAAAACTAAATAAATAAAATGC 361
            | |  |   || ||  |||| ||||   |  | || |
Db    123 GCATGCAGCGCTATTTTATAAAAAATAAAACTACTATATAC 163


RESULT 10
CNS00EVL
LOCUS       CNS00EVL                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1  GI:4949849
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="BACR29B23"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
BASE COUNT      419 a     91 c     60 g    299 t    232 others
ORIGIN

  Query Match             10.6%;  Score 51.8;  DB 17;  Length 1101;
  Best Local Similarity   43.3%;  Pred. No. 4.4;
  Matches   68;  Conservative   30;  Mismatches   59;  Indels    0;  Gaps    0;
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Qy     334 TTATAATAAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTATATATA 393
           :::|:|||  : ||   ||:|: | :       :: :  || |: |: || |||||||:
Db     936 WWWTWATATTWTTATTAAAWTWTATWWATTWATTWWAWTWTATAWTTWTATWTATATATW 995

Qy     394 TGACTCAATATCGNGCATAACGTATTAGTTATGCACTTCTATCATATGGAATAAACATCA 453
           : | | :|||      ||| |||   |||:  | |  |||  :||  ::||:| || :
Db     996 WTAWTAWATATATTTATTAAWWTATATTTTAWAAAWTAATATATWATAWWWTAWATATAW 1055

Qy     454 ATAAGTAATTTCGTNTCCAAAAAAAAAAAAAAAAAAA 490
           |::| | |:||       ||:| |::|||||:|||:
Db    1056 AWWAATTAWTTATATATWTAAWATAWWAAAAAWAAAW 1092


RESULT 11
AJ503961
LOCUS       AJ503961                366 bp    mRNA    linear   EST 09-AUG-2002
DEFINITION  AJ503961 MTAMP Medicago truncatula cDNA clone mtgmadc120040e02,
            mRNA sequence.
ACCESSION   AJ503961
VERSION     AJ503961.1  GI:22084889
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Manthey,K., Bartelsmeier,V., Baier,M.C., Meyer,F., Bartels,D.,
            Bekel,T., Linke,B., Grunwald,U., Franken,P., Kuester,H., Perlick
            ,A.M. and Puehler,A.
  TITLE     Detection of transcript sequences from mycorrhizal roots of the
            model mycorrhiza Medicago truncatula genotype A17 - Glomus mosseae
            using the approach of an EST genome project
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kuester H
            Lehrstuhl fuer Genetik
            Universitaet Bielefeld
            Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="mtgmadc120040e02"
                     /clone_lib="MTAMP"
                     /tissue_type="mycorrhizal roots"
                     /dev_stage="three weeks"
                     /note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI;
                     genotype A17; cDNA was prepared from polyA+ enriched RNA
                     from mycorrhizal roots harvested after three weeks. The
                     cDNA was directionally ligated by MediGenomix into the
                     pGEM-T vector from Promega using GCATGCGGCCGAGGCGGCCGACATG
                     and CTGCAGGCCATTATGGCCGGG adapters. Plasmids containing
                     cDNA inserts were propagated in E. coli DH10B cells."
BASE COUNT      117 a     56 c     76 g    117 t
ORIGIN

  Query Match             10.1%;  Score 49.4;  DB 9;  Length 366;
  Best Local Similarity   68.7%;  Pred. No. 21;
  Matches   68;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy      48 ATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTC 107
           ||   | |  | ||    ||  ||   |||||||||||| |||| ||| |||| ||||||
Db      23 ATTATTTTAGAACACAAAAAAGAAGTGATGGAGAAGAAAACACTTGCTAGCTTGTGCTTC 82

Qy     108 CTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG 146
            |  || | |||||||| | ||| ||||||   ||||||
Db      83 TTTCTCATTGTTCTCTTAGCTGCTCAAGAAGCAGTGGTG 121


RESULT 12
BG453394
LOCUS       BG453394                543 bp    mRNA    linear   EST 16-MAR-2001
DEFINITION  NF090E11LF1F1084 Developing leaf Medicago truncatula cDNA clone
            NF090E11LF 5', mRNA sequence.
ACCESSION   BG453394
VERSION     BG453394.1  GI:13372188
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 543)
  AUTHORS   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula leaf library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 543   Std Error: 0.00
            Plate: 090  row: E  column: 11
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .543
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF090E11LF"
                     /clone_lib="Developing leaf"
                     /tissue_type="leaf"
                     /dev_stage="Pooled developmental"
                     /note="Vector: Lambda Zap; Contains a mixture of very
                     young, developing, mature and senescing leaves."
BASE COUNT      110 a    132 c     86 g    210 t      5 others
ORIGIN

  Query Match             10.1%;  Score 49.4;  DB 12;  Length 543;
  Best Local Similarity   66.7%;  Pred. No. 17;
  Matches   68;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy      45 TTTATATATATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGC 104
           ||| |   | |  | ||    ||  ||   ||||| |||||| |||| ||| |||| |||
Db     363 TTTCTTCTTTTANAACACAAAAAAGAAGTGATGGANAAGAAAACACTTGCTAGCTTGTGC 422

Qy     105 TTCCTCTTCTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG 146
           ||| |  || | |||||||| | ||| ||| ||   ||||||
Db     423 TTCTTTCTCATTGTTCTCTTAGCTGCTCAANAAGCAGTGGTG 464


RESULT 13
BG452703
LOCUS       BG452703                452 bp    mRNA    linear   EST 16-MAR-2001
DEFINITION  NF079E01LF1F1003 Developing leaf Medicago truncatula cDNA clone
            NF079E01LF 5', mRNA sequence.
ACCESSION   BG452703
VERSION     BG452703.1  GI:13371497
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 452)
  AUTHORS   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula leaf library
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 452   Std Error: 0.00
            Plate: 079  row: E  column: 01
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .452
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF079E01LF"
                     /clone_lib="Developing leaf"
                     /tissue_type="leaf"
                     /dev_stage="Pooled developmental"
                     /note="Vector: Lambda Zap; Contains a mixture of very
                     young, developing, mature and senescing leaves."
BASE COUNT      158 a     60 c     89 g    145 t
ORIGIN

  Query Match            10.0%;  Score 49.2;  DB 12;  Length 452;
  Best Local Similarity  70.2%;  Pred. No. 21;
  Matches   66;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy      53 TATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTT 112
           | |  | ||    ||  ||   |||||||||||| |||| ||| |||| |||||| |  |
Db       3 TTTAGAACACAAAAAAGAAGTGATGGAGAAGAAAACACTTGCTAGCTTGTGCTTCTTTCT 62

Qy     113 CTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG 146
           | | |||||||| | ||| ||||||   ||||||
Db      63 CATTGTTCTCTTAGCTGCTCAAGAAGCAGTGGTG 96


RESULT 14
BQ157500
LOCUS       BQ157500                466 bp    mRNA    linear   EST 24-APR-2002
DEFINITION  NF105E08IR1F1067 Irradiated Medicago truncatula cDNA clone
            NF105E08IR 5', mRNA sequence.
ACCESSION   BQ157500
VERSION     BQ157500.1  GI:20294559
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula irradiated library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 466   Std Error: 0.00
            Plate: 105  row: E  column: 08
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .466
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF105E08IR"
                     /clone_lib="Irradiated"
                     /tissue_type="seedlings"
                     /dev_stage="seedling"
                     /note="Vector: Lambda Zap; Seedlings were exposed either
                     to 100 gy gamma or 0.5, 1, 5, or  10 kJ/m2 UV irradiation.
                     Gamma-irradiated samples were harvested at 6,  12, 24 and
                     48 hours after treatment. UV-irradiated samples were
                     harvested  24 hours post-treatment. cDNA was prepared from
                     polyA+ enriched,  pooled samples of equivalent amounts of
                     total RNA from each sample.  The cDNA was directionally
                     ligated into the Uni-Zap XR vector  (Stratagene) and
                     packaged using the Gigapack III Gold packaging  extracts.
                     Phagemids containing cDNA inserts were in vivo excised
                     from  the recombinant Uni-ZAP XR vector using ExAssist
                     helper phage and the  E. coli strain XL1-Blue MRF'
                     (Stratagene). Excised plasmids were  plated using SOLR
                     cells."
BASE COUNT      162 a     64 c     94 g    146 t
ORIGIN

  Query Match            10.0%;  Score 49.2;  DB 14;  Length 466;
  Best Local Similarity  70.2%;  Pred. No. 20;
  Matches   66;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy      53 TATTCATCAATCTAATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTT 112
           | |  | ||    ||  ||   |||||||||||| |||| ||| |||| |||||| |  |
Db      10 TTTAGAACACAAAAAAGAAGTGATGGAGAAGAAAACACTTGCTAGCTTGTGCTTCTTTCT 69

Qy     113 CTTGGTTCTCTTTGTTGCACAAGAAATTGTGGTG 146
           | | |||||||| | ||| ||||||   ||||||
Db      70 CATTGTTCTCTTAGCTGCTCAAGAAGCAGTGGTG 103


RESULT 15
BI269947
LOCUS       BI269947                447 bp    mRNA    linear   EST 18-JUL-2001
DEFINITION  NF017G12IR1F1099 Irradiated Medicago truncatula cDNA clone
            NF017G12IR 5', mRNA sequence.
ACCESSION   BI269947
VERSION     BI269947.1  GI:14877082
KEYWORDS    EST.
SOURCE      barrel medic.
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula irradiated library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: May GD
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7391
            Fax: 580 221 7380
            Email: gdmay@noble.org
            Insert Length: 447   Std Error: 0.00
            Plate: 017  row: G  column: 12
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Medicago truncatula"
                     /db_xref="taxon:3880"
                     /clone="NF017G12IR"
                     /clone_lib="Irradiated"
                     /tissue_type="seedlings"
                     /dev_stage="seedling"
                     /note="Vector: Lambda Zap; Seedlings were exposed either
                     to 100 gy gamma or 0.5, 1, 5, or  10 kJ/m2 UV irradiation.
                     Gamma-irradiated samples were harvested at 6,  12, 24 and
```

48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 157 a 60 c 89 g 141 t
ORIGIN

Query Match 10.0%; Score 49; DB 13; Length 447;
Best Local Similarity 75.3%; Pred. No. 22;
Matches 61; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy      66 AATCAAACTATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTTT 125
           ||  ||   |||||||||||| |||| ||| |||| |||||| |  || | ||||||||
Db      11 AAAGAAGTGATGGAGAAGAAAACACTTGCTAGCTTGTGCTTCTTTCTCATTGTTCTCTTA 70

Qy     126 GTTGCACAAGAAATTGTGGTG 146
           | ||| ||||||   ||||||
Db      71 GCTGCTCAAGAAGCAGTGGTG 91
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Search completed: May 8, 2003, 07:15:44
Job time : 1784.2 secs

GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:17:37 ; Search time 572.217 Seconds
(without alignments)
7018.649 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242
Perfect score: 138
Sequence: 1 AGAACATGTGAGAATTTGGC.....GGTGTACTAAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	138	100.0	406	8	AF319468	AF319468 Medicago
2	88.6	64.2	363	8	AF139018	AF139018 Pisum sat
3	88.6	64.2	468	8	PEADRR230A	L01578 Pea (pi230)
4	88.6	64.2	468	8	PSPI230	X52225 P.sativum p
5	61.4	44.5	494	6	AX252303	AX252303 Sequence
6	58.2	42.2	496	8	AB020613	AB020613 Vigna rad
7	55	39.9	459	8	VUSTORED	X16877 Vigna ungui
c 8	49.2	35.7	380	8	AB049718	AB049718 Pisum sat
9	40	29.0	141	6	A27063	A27063 L.cicera AF
10	40	29.0	141	6	A39547	A39547 Sequence 35
11	40	29.0	141	6	AR050147	AR050147 Sequence
12	40	29.0	141	6	AR130266	AR130266 Sequence
13	40	29.0	141	6	I23722	I23722 Sequence 35
14	39.6	28.7	456	8	PEADRR230B	L01579 Pisum sativ
15	39.6	28.7	456	8	PSPI39	X52224 P.sativum p
c 16	34.2	24.8	160480	2	AC127931	AC127931 Rattus no
17	32.8	23.8	208342	2	AC105077	AC105077 Mus muscu
18	32.4	23.5	110626	9	AC005541	AC005541 Homo sapi
19	32.4	23.5	170723	9	AC013470	AC013470 Homo sapi
20	32	23.2	172255	2	AC101944	AC101944 Mus muscu
c 21	31.8	23.0	161390	9	AC013414	AC013414 Homo sapi
22	31.8	23.0	191989	2	AP005462	AP005462 Oryza sat
c 23	31.6	22.9	133843	8	AC003981	AC003981 Genomic s
24	31.2	22.6	83276	2	AC026631	AC026631 Homo sapi
c 25	31.2	22.6	167293	2	AC022629	AC022629 Homo sapi
c 26	31.2	22.6	195280	9	AC073869	AC073869 Homo sapi
27	30.8	22.3	25560	9	AP000298	AP000298 Homo sapi
28	30.8	22.3	40791	9	AF039907	AF039907 Homo sapi
29	30.8	22.3	100000	9	AP000044	AP000044 Homo sapi
30	30.8	22.3	100000	9	AP000112	AP000112 Homo sapi
31	30.8	22.3	100000	9	AP000188	AP000188 Homo sapi
32	30.8	22.3	141689	2	AC128028	AC128028 Rattus no
c 33	30.8	22.3	186661	2	AC125570	AC125570 Rattus no
34	30.8	22.3	340000	9	AP001716	AP001716 Homo sapi
35	30.6	22.2	141276	2	AC096478	AC096478 Rattus no
36	30.6	22.2	168319	9	AC023282	AC023282 Homo sapi
c 37	30.6	22.2	171799	2	AC099593	AC099593 Mus muscu
38	30.6	22.2	187607	2	AC102122	AC102122 Mus muscu
39	30.6	22.2	198607	2	AC130721	AC130721 Mus muscu
40	30.6	22.2	347162	10	AC084070	AC084070 Mus muscu
c 41	30.4	22.0	1740	9	AB047901	AB047901 Macaca fa
c 42	30.4	22.0	37948	6	AR166758	AR166758 Sequence
c 43	30.4	22.0	99042	2	AC123238	AC123238 Rattus no
44	30.4	22.0	162973	2	AC016307	AC016307 Homo sapi
45	30.4	22.0	163621	9	AC112129	AC112129 Homo sapi

ALIGNMENTS

RESULT 1
AF319468
LOCUS AF319468 406 bp mRNA linear PLN 14-DEC-2000
DEFINITION Medicago sativa antifungal protein precursor, mRNA, complete cds.
ACCESSION AF319468
VERSION AF319468.1 GI:11762085
KEYWORDS .
SOURCE Medicago sativa.
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 406)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakimi,S.

```
  TITLE     Antifungal Polypeptide(s) and Methods for Controlling Plant
            Pathogenic Fungi
  JOURNAL   Patent: US 6121436 19-SEP-2000;
            Monsanto Company; St Louis, MO
REFERENCE   2  (bases 1 to 406)
  AUTHORS   Gao,A.G., Hakimi,S.M., Mittanck,C.A., Wu,Y., Woerner,B.M.,
            Stark,D.M., Shah,D.M., Liang,J. and Rommens,C.M.
  TITLE     Fungal pathogen protection in potato by expression of a plant
            defensin peptide
  JOURNAL   Nat. Biotechnol. 18 (12), 1307-1310 (2000)
  MEDLINE   20553844
   PUBMED   11101813
REFERENCE   3  (bases 1 to 406)
  AUTHORS   Mittanck,C.A., Wu,Y., Hakimi,S.M., Liang,J., Shah,D.M. and Gao,A.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-NOV-2000) Monsanto Company, 700 Chesterfield Parkway,
            St Louis, MO 63198, USA
FEATURES             Location/Qualifiers
     source          1. .406
                     /organism="Medicago sativa"
                     /db_xref="taxon:3879"
     CDS             75. .293
                     /note="alfAFP; defensin"
                     /codon_start=1
                     /product="antifungal protein precursor"
                     /protein_id="AAG40321.1"
                     /db_xref="GI:11762086"
                     /translation="MEKKSLAGLCFLFLVLFVAQEIVVTEARTCENLADKYRGPCFSG
                     CDTHCTTKENAVSGRCRDDFRCWCTKRC"
     sig_peptide     75. .155
     mat_peptide     156. .290
                     /product="antifungal protein"
BASE COUNT      140 a     74 c     78 g    114 t
ORIGIN

  Query Match           100.0%;  Score 138;  DB 8;  Length 406;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-33;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 215

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 275

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    276 TGTACTAAAAGATGTTAA 293


RESULT 2
AF139018
LOCUS       AF139018                363 bp    mRNA    linear   PLN 02-JAN-2001
DEFINITION  Pisum sativum disease resistance response protein 230 precursor
            (DRR230) mRNA, complete cds.
ACCESSION   AF139018
VERSION     AF139018.1  GI:12002298
KEYWORDS    .
SOURCE      Pisum sativum.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Savenstrand,H., Brosche,M. and Strid,A.
  TITLE     Stress-induced disease resistance response protein 230 cDNA from
            Pisum sativum cv. Greenfeast
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Savenstrand,H., Brosche,M. and Strid,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-1999) Biochemistry and Biophysics, Goteborg
            University, Medicinaregatan 9c, P.O. Box 462, Goteborg S-40530,
            Sweden
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Pisum sativum"
                     /cultivar="Greenfeast"
                     /db_xref="taxon:3888"
     gene            1. .363
                     /gene="DRR230"
     CDS             56. .274
                     /gene="DRR230"
                     /note="ozone-induced; similar to the Pisum sativum cv.
                     Alaska product encoded by GenBank Accession Number L01578"
                     /codon_start=1
                     /product="disease resistance response protein 230
                     precursor"
                     /protein_id="AAG43285.1"
                     /db_xref="GI:12002299"
                     /translation="MEKKSLACLSFLLLVLFIAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
BASE COUNT      113 a     68 c     74 g    108 t
ORIGIN

  Query Match           64.2%;  Score 88.6;  DB 8;  Length 363;
  Best Local Similarity  78.5%;  Pred. No. 1.9e-17;
  Matches  106;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
          ||||||||||||||||| | |  ||||| |||| |||||| .|||| ||||||  ||||
Db    140 ACATGTGAGAATTTGGCTGGTTCATATAAGGGAGTATGCTTCGGTGGATGTGACCGTCAC 199

Qy     64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
          || | |||  ||||| |||| |||| || || || ||||| ||||| ||||| |||||
Db    200 TGTAGAACACAAGAGGGCGCAATTAGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGC 259

Qy    124 ACTAAAAGATGTTAA 138
          |||||||  ||||||
Db    260 ACTAAAAACTGTTAA 274


RESULT 3
PEADRR230A
LOCUS       PEADRR230A              468 bp    mRNA    linear   PLN 11-FEB-2002
DEFINITION  Pea (pi230) disease resistance response protein 230 (DRR230-a)
            mRNA, complete cds.
ACCESSION   L01578 S88685
VERSION     L01578.1  GI:169073
KEYWORDS    cysteine-rich protein; disease resistance response protein 230;
            pathogenesis-related protein.
SOURCE      Pisum sativum.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 468)
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
   PUBMED   1799696
COMMENT     On Feb 8, 2002 this sequence version replaced gi:247416.
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Pisum sativum"
                     /strain="Alaska"
                     /db_xref="taxon:3888"
                     /tissue_type="pod tissue treated with Fusarium solani
                     conidia"
                     /dev_stage="immature"
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     gene            1. .468
                     /gene="DRR230-a"
     CDS             78. .296
                     /gene="DRR230-a"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /note="pi230"
                     /codon_start=1
                     /evidence=experimental
                     /product="disease resistance response protein"
                     /protein_id="AAA79117.1"
                     /db_xref="GI:169074"
                     /translation="MEKKSLACLSFLLLVLFVAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
     mat_peptide     159. .293
                     /gene="DRR230-a"
                     /product="disease resistance response protein"
                     /function="unknown"
                     /note="determined by in vitro cleavage with microsomal
                     membranes"
                     /evidence=experimental
BASE COUNT      153 a     88 c     84 g    143 t
ORIGIN

  Query Match           64.2%;  Score 88.6;  DB 8;  Length 468;
  Best Local Similarity   78.5%;  Pred. No. 1.8e-17;
  Matches  106;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
          |||||||||||||||| | |  ||||| ||||  ||||||  |||| ||||||  ||||
Db    162 ACATGTGAGAATTTGGCTGGTTCATATAAGGGAGTATGCTTCGGTGGATGTGACCGTCAC 221

Qy     64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
          || | |||  |||||  |||| |||| || || || ||||| ||||| ||||| |||||
Db    222 TGTAGAACACAAGAGGGCGCAATTAGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGC 281

Qy    124 ACTAAAAGATGTTAA 138
          |||||||  ||||||
Db    282 ACTAAAAACTGTTAA 296


RESULT 4
PSPI230
LOCUS       PSPI230                 468 bp    mRNA    linear   PLN 09-AUG-2002
DEFINITION  P.sativum pI230 mRNA.
ACCESSION   X52225
VERSION     X52225.1  GI:22208748
KEYWORDS    secreted protein.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
REFERENCE   2  (bases 1 to 468)
  AUTHORS   Chiang,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1990) Chiang C., Washington State University,
            Dept. of Plant Phatology, Pullman, WA 99164-6430, USA
FEATURES             Location/Qualifiers
     source          1. .468
                     /organism="Pisum sativum"
                     /db_xref="taxon:3888"
                     /tissue_type="endocarp"
     gene            1. .468
                     /gene="pI230"
     CDS             78. .296
                     /gene="pI230"
                     /codon_start=1
                     /protein_id="CAA36474.1"
                     /db_xref="GI:22208749"
                     /translation="MEKKSLACLSFLLLVLFVAQEIVVSEANTCENLAGSYKGVCFGG
                     CDRHCRTQEGAISGRCRDDFRCWCTKNC"
     sig_peptide     78. .158
                     /gene="pI230"
     mat_peptide     159. .293
                     /gene="pI230"
                     /product="unnamed"
BASE COUNT      153 a     88 c     84 g    143 t
ORIGIN

  Query Match           64.2%;  Score 88.6;  DB 8;  Length 468;
  Best Local Similarity   78.5%;  Pred. No. 1.8e-17;
  Matches  106;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
          |||||||||||||||| | |  ||||| ||||  ||||||  |||| ||||||  ||||
Db    162 ACATGTGAGAATTTGGCTGGTTCATATAAGGGAGTATGCTTCGGTGGATGTGACCGTCAC 221

Qy     64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
          || | |||  |||||  |||| |||| || || || ||||| ||||| ||||| |||||
Db    222 TGTAGAACACAAGAGGGCGCAATTAGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGC 281

Qy    124 ACTAAAAGATGTTAA 138
          |||||||  ||||||
Db    282 ACTAAAAACTGTTAA 296


RESULT 5
AX252303
LOCUS       AX252303                494 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168887.
ACCESSION   AX252303
VERSION     AX252303.1  GI:15985643
KEYWORDS    .
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   Jung,R. and Kinney,A.J.
  TITLE     Hypoallergenic transgenic soybeans
  JOURNAL   Patent: WO 0168887-A 5 20-SEP-2001;
            E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
            INTERNATIONAL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .494
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
BASE COUNT      153 a     97 c    103 g    134 t     7 others
ORIGIN

  Query Match           44.5%;  Score 61.4;  DB 6;  Length 494;
  Best Local Similarity   70.2%;  Pred. No. 7.8e-09;
  Matches   99;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
          || || |||||  |||| |||| ||| ||||| ||||||||      | |  | || ||
Db    133 ACTTGCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGAT 192

Qy     58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
          ||||||||  | ||||||| ||    | || || || || |||||||| || |||||
Db    193 GATCACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGT 252

Qy    118 TGGTGTACTAAAAGATGTTAA 138
          |||||  || ||||  ||||||
Db    253 TGGTGCACCAAAAACTGTTAA 273
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RESULT 6
AB020613
LOCUS       AB020613                496 bp    mRNA    linear   PLN 05-JAN-2002
DEFINITION  Vigna radiata mRNA for PDF1, complete cds.
ACCESSION   AB020613
VERSION     AB020613.1  GI:18146787
KEYWORDS    PDF1.
SOURCE      Vigna radiata (strain:B20F5 9-3-2-2) immature seed cDNA to mRNA,
            clone_lib:B20 clone:pDF-1.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1
  AUTHORS   Ishimoto,M. and Kaga,A.
  TITLE     Mungbean defensin
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 496)
  AUTHORS   Ishimoto,M. and Kaga,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-DEC-1998) Masao Ishimoto, Chugoku National
            Agricultural Experiment Station, Laboratory of Plant Biotechnology;
            6-12-1 Nishifukatsu, Fukuyama, Hiroshima 721-8514, Japan
            (E-mail:ishimoto@cgk.affrc.go.jp, Tel:+81-849-234100(ex.231),
            Fax:+81-849-247893)
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Vigna radiata"
                     /strain="B20F5 9-3-2-2"
                     /db_xref="taxon:157791"
                     /clone="pDF-1"
                     /tissue_type="immature seed"
                     /clone_lib="B20"
     gene            1. .496
                     /gene="pDF1"
     CDS             46. .273
                     /gene="pDF1"
                     /codon_start=1
                     /product="PDF1"
                     /protein_id="BAB82453.1"
                     /db_xref="GI:18146788"
                     /translation="MEKKSLAGLCFLFLVLFVAQEVMVQTEAKTCENLANTYRGPCFT
                     TGSCDDHCKNKEHLRSGRCRDDFRCWCTRNC"
     polyA_site      496
                     /gene="pDF1"
                     /note="17 a nucleotides"
BASE COUNT      148 a    104 c    106 g    138 t
ORIGIN

  Query Match             42.2%;  Score 58.2;  DB 8;  Length 496;
  Best Local Similarity   68.8%;  Pred. No. 8.1e-08;
  Matches   97;  Conservative    0;  Mismatches   38;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || || |||||  ||||  |||  || ||||| ||||||||      | |  | || ||
Db     133 ACTTGCGAGAACCTGGCGAATACTTACAGGGGTCCATGCTTCACCACTGGCAGCTGCGAT 192

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             ||||||||  | ||||||  ||      ||||| ||||| |||||||| ||||| ||
Db     193 GATCACTGCAAGAACAAAGAACACTTGAGGAGTGGCAGGTGCAGGGACGATTTCCGGTGT 252

Qy     118 TGGTGTACTAAAAGATGTTAA 138
           ||||| |||| ||  ||||||
Db     253 TGGTGCACTAGAAACTGTTAA 273


RESULT 7
VUSTORED
LOCUS       VUSTORED                459 bp    mRNA    linear   PLN 12-SEP-1993
DEFINITION  Vigna unguiculata cDNA for stored cotyledon mRNA.
ACCESSION   X16877
VERSION     X16877.1  GI:22075
KEYWORDS    .
SOURCE      Vigna radiata.
  ORGANISM  Vigna radiata
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Vigna.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Yamauchi,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-1989) Yamauchi D., Dept of Biology, Tokyo
            Metropolitan University, Fukazawa 2-1, Setagaya-ku, Tokyo 158,
            Japan
REFERENCE   2  (bases 1 to 459)
  AUTHORS   Ishibashi,N., Yamauchi,D. and Minamikawa,T.
  TITLE     Stored mRNA in cotyledons of Vigna unguiculata seeds: nucleotide
            sequence of cloned cDNA for a stored mRNA and induction of its
            synthesis by precocious germination
  JOURNAL   Plant Mol. Biol. 15 (1), 59-64 (1990)
  MEDLINE   91355865
   PUBMED   2103443
FEATURES             Location/Qualifiers
     source          1. .459
                     /organism="Vigna radiata"
                     /db_xref="taxon:157791"
                     /clone="pSAS10"
                     /tissue_type="cotyledon"
                     /clone_lib="lambda gt10"
                     /dev_stage="seed"
     CDS             14. .241
                     /note="pSAS10 ORF"
                     /codon_start=1
                     /protein_id="CAA34760.1"
                     /db_xref="GI:22076"
                     /db_xref="SWISS-PROT:P18646"
                     /translation="MEKKSIAGLCFLFLVLFVAQEVVVQSEAKTCENLVDTYRGPCFT
                     TGSCDDHCKNKEHLLSGRCRDDVRCWCTRNC"
BASE COUNT      136 a     91 c     99 g    133 t
ORIGIN

  Query Match             39.9%;  Score 55;  DB 8;  Length 459;
  Best Local Similarity   67.4%;  Pred. No. 8.4e-07;
  Matches   95;  Conservative    0;  Mismatches   40;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || || |||||  |||  |||| ||| ||||| || |||||      | |  | || ||
Db     101 ACTTGCGAGAACCTGGTGGATACATACAGGGGTCCGTGCTTCACCACTGGGAGCTGCGAT 160

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             ||||||||  | ||||||  ||     | ||||| ||||| ||||| ||  |||| ||
Db     161 GATCACTGCAAGAACAAAGAACACTTGCTGAGTGGCAGGTGCAGGGATGATGTCCGGTGT 220

Qy     118 TGGTGTACTAAAAGATGTTAA 138
           ||||| || | ||  ||||||
Db     221 TGGTGCACCAGAAACTGTTAA 241


RESULT 8
AB049718/c
LOCUS       AB049718                380 bp    mRNA    linear   PLN 08-JUN-2001
DEFINITION  Pisum sativum ssa-8 mRNA for putative senescence-associated
            protein, complete cds.
ACCESSION   AB049718
VERSION     AB049718.1  GI:13359440
KEYWORDS    .
SOURCE      Pisum sativum (cultivar:Ichihara wase) immatured pods pods cDNA to
            mRNA.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
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REFERENCE   1  (sites)
  AUTHORS   Pariasca,J.A.T., Sunaga,A., Miyazaki,T., Hisaka,H., Sonoda,M.,
            Nakagawa,H. and Sato,T.
  TITLE     Cloning of cDNAs encoding senescence-associated genes, ACC synthase
            and ACC oxidase from stored snow pea pods (Pisum sativum L. var
            saccharatum) and their expression during pod storage
  JOURNAL   Postharvest Biology and Technology 22, 239-247 (2001)
REFERENCE   2  (bases 1 to 380)
  AUTHORS   Pariasca,J.A. and Sato,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-2000) Takahide Sato, Chiba University, Faculty of
            Horticulture; 648 Matsudo, Matsudo, Chiba 271-8510, Japan
            (E-mail:sato@midori.h.chiba-u.ac.jp, Tel:81-47-308-8863)
FEATURES             Location/Qualifiers
     source          1. .380
                     /organism="Pisum sativum"
                     /cultivar="Ichihara wase"
                     /db_xref="taxon:3888"
                     /tissue_type="pods"
                     /dev_stage="immatured pods"
                     /country="Japan: Chiba, Matsudo"
                     /note="cDNAs isolated from a 5-day stored pod cDNA library
                     by differential screening"
     gene            1. .380
                     /gene="ssa-8"
     CDS             98. .370
                     /gene="ssa-8"
                     /codon_start=1
                     /product="putative senescence-associated protein"
                     /protein_id="BAB33416.1"
                     /db_xref="GI:13359441"
                     /translation="MHDIEYTHNSQSRIQHTGAVQILHIIVFIHIIWSFIFLHILSLR
                     VGENWINSFECTSSENHPCTSHSVCARCSCNVCCSYHLGCMVPVFY"
BASE COUNT      120 a     78 c     64 g    118 t
ORIGIN

  Query Match           35.7%;  Score 49.2;  DB 8;  Length 380;
  Best Local Similarity   70.2%;  Pred. No. 5.8e-05;
  Matches   66;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy      45 TAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGA 104
           | ||   ||  |||  || ||||  | ||| ||| ||  | | ||||| ||||| |||||
Db     339 TGGTAACTGCAACAAACATTGCAGGAACAACGAGCACATACTGAGTGGGAGGTGCAGGGA 280

Qy     105 CGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 138
           || || ||||.|||||| |||  ||  ||||||
Db     279 TGATTTTCGCTGCTGGTGCACTCGAAACTGTTAA 246


RESULT 9
A27063
LOCUS       A27063                   141 bp    DNA     linear   PAT 12-JUN-1995
DEFINITION  L.cicera AFP sequence.
ACCESSION   A27063
VERSION     A27063.1  GI:1247357
KEYWORDS    .
SOURCE      Lathyrus cicera.
  ORGANISM  Lathyrus cicera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Lathyrus.
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="Lathyrus cicera"
                     /db_xref="taxon:3856"
BASE COUNT       43 a     30 c     32 g     33 t      3 others
ORIGIN

  Query Match           29.0%;  Score 40;  DB 6;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.049;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  |  | ||||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 10
A39547
LOCUS       A39547                   141 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 35 from Patent WO9416076.
ACCESSION   A39547
VERSION     A39547.1  GI:2295840
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Dubock,A.C., Powell,K.A. and Rees,S.B.
  TITLE     ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
  JOURNAL   Patent: WO 9416076-A 35 21-JUL-1994;
            ZENECA LTD (GB)
COMMENT     Other publication AU 5820494 940815.
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unidentified"
                     /db_xref="taxon:32644"
BASE COUNT       43 a     30 c     32 g     33 t      3 others
ORIGIN

  Query Match           29.0%;  Score 40;  DB 6;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.049;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  |  | ||||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 11
AR050147
LOCUS       AR050147                 141 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 35 from patent US 5824869.
ACCESSION   AR050147
VERSION     AR050147.1  GI:5972139
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
            Terras,F.R.G. and Vanderleyden,J.
  TITLE     Biocidal proteins
  JOURNAL   Patent: US 5824869-A 35 20-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
BASE COUNT       43 a     30 c     32 g     33 t      3 others
ORIGIN
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  Query Match             29.0%;  Score 40;  DB 6;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.049;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  | | |||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 12
AR130266
LOCUS       AR130266                 141 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 35 from patent US 6187904.
ACCESSION   AR130266
VERSION     AR130266.1  GI:14118163
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
            Terras,F.R.G. and Vanderleyden,J.
  TITLE     Biocidal proteins
  JOURNAL   Patent: US 6187904-A 35 13-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
BASE COUNT       43 a     30 c     32 g     33 t      3 others
ORIGIN

  Query Match             29.0%;  Score 40;  DB 6;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.049;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  | | |||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 13
I23722
LOCUS       I23722                   141 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 35 from patent US 5538525.
ACCESSION   I23722
VERSION     I23722.1  GI:1603592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 141)
  AUTHORS   Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
            Terras,F.R.G. and Vanderleyden,J.
  TITLE     Biocidal proteins
  JOURNAL   Patent: US 5538525-A 35 23-JUL-1996;
FEATURES             Location/Qualifiers
     source          1. .141
                     /organism="unknown"
BASE COUNT       43 a     30 c     32 g     33 t      3 others
ORIGIN

  Query Match             29.0%;  Score 40;  DB 6;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.049;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  | | |||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 14
PEADRR230B
LOCUS       PEADRR230B               456 bp    mRNA    linear   PLN 11-FEB-2002
DEFINITION  Pisum sativum disease resistance response protein 39 (DRR230-b)
            mRNA, complete cds.
ACCESSION   L01579 S88682
VERSION     L01579.1  GI:169075
KEYWORDS    cysteine-rich protein; disease resistance response protein 39;
            pathogenesis-related protein.
SOURCE      Pisum sativum (strain Alaska) cDNA to mRNA.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 456)
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
   PUBMED   1799696
COMMENT     On Feb 8, 2002 this sequence version replaced gi:247414.
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Pisum sativum"
                     /strain="Alaska"
                     /db_xref="taxon:3888"
                     /tissue_type="pod tissue treated with Fusarium solani
                     conidia."
                     /dev_stage="immature"
     gene            1. .456
                     /gene="DRR230-b"
     CDS             69. .293
                     /gene="DRR230-b"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /codon_start=1
                     /evidence=experimental
                     /product="disease resistance response protein 39"
                     /protein_id="AAA79118.1"
                     /db_xref="GI:169076"
                     /translation="MEKKSLAALSFLLLLVLFVAQEIVVTEANTCEHLADTYRGVCFT
                     NASCDDHCKNKAHLISGTCHDWKCFCTQNC"
     mat_peptide     153. .290
                     /gene="DRR230-b"
                     /product="disease resistance response protein"
                     /function="unknown"
                     /standard_name="pathogenesis related protein"
                     /note="citocleavage determined by homology with pi230;
                     putative"
BASE COUNT      155 a     81 c     79 g    141 t
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ORIGIN

  Query Match             28.7%;  Score 39.6;  DB 8;  Length 456;
  Best Local Similarity   67.6%;  Pred. No. 0.065;
  Matches   73;  Conservative    0;  Mismatches   29;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || |||||| ||||||| |||| ||| ||||||  ||||||      |  | | |||||
Db     156 ACTTGTGAGCATTTGGCTGATACATACAGGGGAGTATGCTTCACGAATGCTAGCTGTGAT 215

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGAC 105
             ||||||||  | ||||| | ||  | | ||||| | |||    |||
Db     216 GATCACTGCAAGAACAAAGCGCACTTAATCAGTGGCACGTGCCATGAC 263


RESULT 15
PSPI39
LOCUS       PSPI39                   456 bp    mRNA    linear   PLN 09-AUG-2002
DEFINITION  P.sativum pI39 mRNA.
ACCESSION   X52224
VERSION     X52224.1  GI:22208744
KEYWORDS    secreted protein.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1
  AUTHORS   Chiang,C.C. and Hadwiger,L.A.
  TITLE     The Fusarium solani-induced expression of a pea gene family
            encoding high cysteine content proteins
  JOURNAL   Mol. Plant Microbe Interact. 4 (4), 324-331 (1991)
  MEDLINE   92190628
REFERENCE   2  (bases 1 to 456)
  AUTHORS   Chiang,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1990) Chiang C., Washington State University,
            Dept. of Plant Phatology, Pullman, WA 99164-6430, USA
FEATURES             Location/Qualifiers
     source          1. .456
                     /organism="Pisum sativum"
                     /db_xref="taxon:3888"
                     /tissue_type="endocarp"
     gene            1. .456
                     /gene="pI39"
     CDS             69. .293
                     /gene="pI39"
                     /codon_start=1
                     /protein_id="CAA36473.1"
                     /db_xref="GI:22208745"
                     /translation="MEKKSLAALSFLLLLVLFVAQEIVVTEANTCEHLADTYRGVCFT
                     NASCDDHCKNKAHLISGTCHDWKCFCTQNC"
     sig_peptide     69. .152
                     /gene="pI39"
     mat_peptide     153. .290
                     /gene="pI39"
                     /product="unnamed"
BASE COUNT      155 a     81 c     79 g    141 t
ORIGIN

  Query Match             28.7%;  Score 39.6;  DB 8;  Length 456;
  Best Local Similarity   67.6%;  Pred. No. 0.065;
  Matches   73;  Conservative    0;  Mismatches   29;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || |||||| ||||||| |||| ||| ||||||  ||||||      |  | | |||||
Db     156 ACTTGTGAGCATTTGGCTGATACATACAGGGGAGTATGCTTCACGAATGCTAGCTGTGAT 215

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGAC 105
             ||||||||  | ||||| | ||  | | ||||| | |||    |||
Db     216 GATCACTGCAAGAACAAAGCGCACTTAATCAGTGGCACGTGCCATGAC 263
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GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

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Sequence: 1 AGAACATGTGAGAATTTGGC.....GGTGTACTAAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	138	100.0	250	19	AAV39187	Alfalfa plant anti
	2	138	100.0	490	19	AAV39186	Antifungal polypep
	3	138	100.0	507	19	AAV39195	Antifungal polypep
	4	119.4	86.5	200	19	AAV39190	Antifungal polypep
	5	117.8	85.4	327	19	AAV39194	Antifungal polypep
	6	88.6	64.2	468	21	AAZ49412	Pea Defensin prote
	7	86.6	62.8	293	19	AAV39191	Antifungal polypep
	8	61.4	44.5	494	22	AAD17530	Soybean Gly m2 pro
	9	40	29.0	141	15	AAQ70126	Antimicrobial Lc-A
c	10	39	28.3	47	19	AAV39197	Antifungal polypep
	11	32.2	23.3	138	14	AAQ38648	Encodes antifungal
c	12	30.4	22.0	37948	20	AAZ06831	Photorhabdus lumin
c	13	30	21.7	2172	24	AAS62653	cDNA sequence #440
c	14	29	21.0	276	16	AAT24882	Human gene signatu
	15	29	21.0	1937	24	AAS62577	cDNA sequence #364
c	16	29	21.0	1082138	21	AAF22305	Arabidopsis thalia
	17	28.8	20.9	15109	18	AAV74355	Staphylococcus aur
	18	28.6	20.7	1024	21	AAC41895	Arabidopsis thalia
	19	28.6	20.7	1400	21	AAA15484	16S rRNA sequence
	20	28.6	20.7	1446	21	AAA15485	16S rRNA sequence
	21	28.6	20.7	1544	22	AAS11030	Treponema palladiu
	22	28.6	20.7	7328	21	AAF20874	Human bradykinin r
	23	28.6	20.7	7328	21	AAF20878	Human bradykinin r
	24	28.6	20.7	7328	21	AAF20887	Human bradykinin r
	25	28.6	20.7	7328	21	AAA34752	Human adenosine re
	26	28.6	20.7	7328	21	AAA34756	Human adenosine re
	27	28.6	20.7	7328	21	AAA34765	Human adenosine re
	28	28.6	20.7	48333	21	AAF21451	Human bradykinin r
	29	28.6	20.7	117609	21	AAF21435	Human receptor-rel
c	30	28.4	20.6	1277	24	ABL50367	Human vascular epi
c	31	28.4	20.6	1418	21	AAC59660	Human secreted pro
c	32	28.4	20.6	2432	22	AAH17679	Human cDNA sequenc
	33	28.4	20.6	4504	23	ABL25672	Drosophila melanog
	34	28.4	20.6	5414	23	ABL25674	Drosophila melanog
c	35	28.2	20.4	2997	17	AAT11641	Murine osteogenic
c	36	28.2	20.4	2997	21	AAA59899	Murine OP-1 downst
c	37	28	20.3	1503900	22	AAK95240	Human neuregulin-1
c	38	28	20.3	1503900	22	AAK96733	Human neuregulin-1
c	39	27.6	20.0	342	24	ABQ67413	Listeria innocua D
c	40	27.6	20.0	2539	24	ABI99857	Mouse ischaemic co
c	41	27.6	20.0	2927	23	ABL13202	Drosophila melanog
	42	27.6	20.0	5220	23	ABL28025	Drosophila melanog
	43	27.6	20.0	8440	23	ABL28024	Drosophila melanog
	44	27.6	20.0	32249	22	AAL04676	Human reproductive
	45	27.6	20.0	32249	23	ABL97583	Human testicular a

ALIGNMENTS

RESULT 1
AAV39187
ID AAV39187 standard; DNA; 250 BP.
XX
AC AAV39187;
XX
DT 25-SEP-1998 (first entry)
XX
DE Alfalfa plant antifungal polypeptide AlfALFP1 encoding DNA.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS Medicago sativa.
XX
FH Key Location/Qualifiers
FT CDS 105..242
FT /*tag= a
FT /product= "mature AlfALFP1"
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX

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DR   WPI; 1998-348537/30.
DR   P-PSDB; AAW61964.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 3; Page 78; 97pp; English.
XX
CC   This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC   alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2  are
CC   useful to control plant fungi, especially pathogenic fungi, by
CC   transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 250 BP; 73 A; 48 C; 64 G; 65 T; 0 other;

  Query Match           100.0%;  Score 138;  DB 19;  Length 250;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-39;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 224

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    225 TGTACTAAAAGATGTTAA 242


RESULT 2
AAV39186
ID   AAV39186 standard; DNA; 490 BP.
XX
AC   AAV39186;
XX
DT   01-OCT-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP1 encoding cDNA.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ss.
XX
OS   Medicago sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..293
FT                   /*tag=  a
FT                   /transl_except= (pos:129..131, aa:Glu)
FT                   /product= "AlfAFP1 polypeptide"
FT   sig_peptide     75..155
FT                   /*tag=  b
FT   mat_peptide     156..290
FT                   /*tag=  c
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
DR   P-PSDB; AAW61967.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 5; Fig 1; 97pp; English.
XX
CC   This cDNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC   alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2  are
CC   useful to control plant fungi, especially pathogenic fungi, by
CC   transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 490 BP; 182 A; 85 C; 85 G; 136 T; 2 other;

  Query Match           100.0%;  Score 138;  DB 19;  Length 490;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-39;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
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Db    156 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 215

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 275

Qy    121 TGTACTAAAAGATGTTAA 138
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Db    276 TGTACTAAAAGATGTTAA 293


RESULT 3
AAV39195
ID   AAV39195 standard; DNA; 507 BP.
XX
AC   AAV39195;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP1 mature sequence encoding DNA.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
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KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS   Medicago sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             173..310
FT                   /*tag= a
FT                   /product= "mature AlfALFP1"
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
DR   P-PSDB; AAW61964.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 5; Page 77; 97pp; English.
XX
CC   This DNA encodes an antifungal polypeptide, AlfAFP1 isolated from
CC   alfalfa plants (Medicago). The polypeptides AlfAFP1 and AlfAFP2  are
CC   useful to control plant fungi, especially pathogenic fungi, by
CC   transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 507 BP; 181 A; 85 C; 102 G; 136 T; 3 other;

  Query Match             100.0%;  Score 138;  DB 19;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-39;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     173 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 232

Qy      61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     233 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 292

Qy     121 TGTACTAAAAGATGTTAA 138
           ||||||||||||||||||
Db     293 TGTACTAAAAGATGTTAA 310


RESULT 4.
AAV39190
ID   AAV39190 standard; DNA; 200 BP.
XX
AC   AAV39190;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP2 5' region.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS   Medicago sativa.
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 18; Page 75; 97pp; English.
XX
CC   This sequence represents the 5' region of the DNA encoding an antifungal
CC   polypeptide, AlfAFP2 isolated from alfalfa plants (Medicago). The
CC   polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
CC   especially pathogenic fungi, by transforming plant cells with a vector
CC   comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
CC   antifungally effective amounts of the polypeptide. Such transformed
CC   plants may be e.g. apple, wheat, cotton and especially potato.
CC   Micro-organisms may also be transformed to produce the polypeptides, and
CC   applied to plants to control plant fungi. The polypeptides can also be
CC   included with a suitable solvent in antifungal compositions and these can
CC   be administered to plants to control plant fungi. Such compositions and
CC   genetically engineered plants may also contain additional molecules e.g.
CC   the compositions can contain other antifungal agents or the plants
CC   contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC   proteins. The polypeptides are also useful to prepare antibodies useful
CC   to detect polypeptides or isolate other alfalfa plant antifungal protein
CC   antigens. The nucleic acids are useful to produce polypeptides and
CC   transgenic plants and as probes or primers in nucleic acid hybridisation
CC   e.g. to detect complementary sequences in samples, and to prepare mutants
CC   or isolate similar sequences from related species.
XX
SQ   Sequence 200 BP; 48 A; 36 C; 65 G; 50 T; 1 other;

  Query Match             86.5%;  Score 119.4;  DB 19;  Length 200;
  Best Local Similarity   99.2%;  Pred. No. 5.7e-33;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 139

Qy      61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     140 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 199

Qy     121 T 121
           |
Db     200 T 200


RESULT 5
```

```
AAV39194
ID   AAV39194 standard; DNA; 327 BP.
XX
AC   AAV39194;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP2 3' region.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS   Medicago sativa.
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 18; Page 77; 97pp; English.
XX
CC   This sequence represents the 3' region of the DNA encoding an antifungal
CC   polypeptide, AlfAFP2 isolated from alfalfa plants (Medicago). The
CC   polypeptides AlfAFP1 and AlfAFP2 are useful to control plant fungi,
CC   especially pathogenic fungi, by transforming plant cells with a vector
CC   comprising sequences encoding AlfAFP1 or AlfAFP2 to allow expression of
CC   antifungally effective amounts of the polypeptide. Such transformed
CC   plants may be e.g. apple, wheat, cotton and especially potato.
CC   Micro-organisms may also be transformed to produce the polypeptides, and
CC   applied to plants to control plant fungi. The polypeptides can also be
CC   included with a suitable solvent in antifungal compositions and these can
CC   be administered to plants to control plant fungi. Such compositions and
CC   genetically engineered plants may also contain additional molecules e.g.
CC   the compositions can contain other antifungal agents or the plants
CC   contain DNA encoding insecticidal (e.g. Bacillus thuringiensis)
CC   proteins. The polypeptides are also useful to prepare antibodies useful
CC   to detect polypeptides or isolate other alfalfa plant antifungal protein
CC   antigens. The nucleic acids are useful to produce polypeptides and
CC   transgenic plants and as probes or primers in nucleic acid hybridisation
CC   e.g. to detect complementary sequences in samples, and to prepare mutants
CC   or isolate similar sequences from related species.
XX
SQ   Sequence 327 BP; 125 A; 49 C; 60 G; 91 T; 2 other;

  Query Match             85.4%;  Score 117.8;  DB 19;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 2.6e-32;
  Matches  122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      10 GAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 69
           |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 GAGAATTTGGCGGATAAGTATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 60

Qy      70 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 129
           |||||||||||||||||||||||||||||||||| ||||| || || | ||||||||||
Db      61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy     130 AGATGTTAA 138
           |||||||||
Db     121 AGATGTTAA 129
```

```
RESULT 6
AAZ49412
ID   AAZ49412 standard; cDNA; 468 BP.
XX
AC   AAZ49412;
XX
DT   04-APR-2000  (first entry)
XX
DE   Pea Defensin protein Drr230, encoding cDNA.
XX
KW   Transgenic plant; disease resistance; DRR206; defensin; Drr230; PR10.1;
KW   chitinase; recombinant expression system; Pea; Canola; Blackleg fungus;
KW   CaMV 35S inducible promoter; T-DNA; bacterial/fungal pathogen;
KW   Leptosphaeria maculans; Rhizoctonia solani; Sclerotinia sclerotiorum; ds.
XX
OS   Pisum sativum.
XX
FH   Key             Location/Qualifiers
FT   CDS             78..296
FT                   /*tag= a
FT                   /product= "Pea Defensin protein, Drr230"
FT                   /note= "Confers resistance against fungal and bacterial
FT                   pathogens"
XX
PN   WO200001824-A2.
XX
PD   13-JAN-2000.
XX
PF   02-JUL-1999;   99WO-CA00608.
XX
PR   03-JUL-1998;   98CA-2242116.
PR   06-JUL-1998;   98US-0091751.
XX
PA   (UYMA-) UNIV MANITOBA.
XX
PI   Fristensky B,  Wang Y;
XX
DR   WPI; 2000-126938/11.
DR   P-PSDB; AAY44509.
XX
PT   Recombinant expression system for expressing DRR206 or defensin, used
PT   to produce pathogen resistant Brassica napus  -
XX
PS   Claim 11; Fig 9; 39pp; English.
XX
CC   The present sequence is the cDNA encoding defensin protein, derived from
CC   the clone Drr230 of Pea. This sequence is strongly induced by bacterial
CC   and fungal pathogens like, blackleg fungus. This gene is used in a
CC   recombinant expression system, capable of transforming plants like,
CC   Canola (Brassica napus), under the constitutive control of CaMV 35S
CC   inducible promoter, responsive to pathogen infections. T-DNA sequence is
CC   also present, for integration of the expression system into the plant
CC   genome. Transgenic plants expressing DRR206 and defensin protein,
CC   inhibited fungal growth in-vitro and are resistant to pathogenic
CC   infections of Rhizoctonia solani, Leptosphaeria maculans and Sclerotinia
CC   sclerotiorum.
XX
SQ   Sequence 468 BP; 153 A; 88 C; 84 G; 143 T; 0 other;

  Query Match             64.2%;  Score 88.6;  DB 21;  Length 468;
  Best Local Similarity   78.5%;  Pred. No. 9e-22;
  Matches  106;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
           |||||||||||||||| | |  ||||| ||||  ||||||  |||| ||||||  ||||
Db     162 ACATGTGAGAATTTGGCTGGTTCATATAAGGGAGTATGCTTCGGTGGATGTGACCGTCAC 221

Qy      64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
           || | |||  |||||  |||| |||| || || || ||||| ||||| ||||| |||||
Db     222 TGTAGAACACAAGAGGGCGCAATTAGCGGCAGATGCAGGGATGACTTTCGCTGTTGGTGC 281

Qy     124 ACTAAAAGATGTTAA 138
```

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          ||||||| ||||||
Db    282 ACTAAAAACTGTTAA 296


RESULT 7
AAV39191
ID   AAV39191 standard; DNA; 293 BP.
XX
AC   AAV39191;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Antifungal polypeptide AlfAFP2 coding sequence.
XX
KW   Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW   plant pathogenic fungus; AlfAFP1; AlfAFP2; ds.
XX
OS   Medicago sativa.
XX
PN   WO9826083-A1.
XX
PD   18-JUN-1998.
XX
PF   11-DEC-1997;   97WO-US22662.
XX
PR   13-DEC-1996;   96US-0766355.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Hakimi S,  Liang J,  Rosenberger CA,  Shah DM,  Wu YS;
XX
DR   WPI; 1998-348537/30.
XX
PT   Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT   - used to control plant pathogenic fungi and to produce transformed
PT   plants with increased fungal resistance
XX
PS   Claim 18; Page 75; 97pp; English.
XX
CC   This represents a coding sequence of an antifungal polypeptide, AlfAFP2
CC   isolated from alfalfa plants (Medicago). The polypeptides AlfAFP1 and
CC   AlfAFP2 are useful to control plant fungi, especially pathogenic fungi,
CC   by transforming plant cells with a vector comprising sequences encoding
CC   AlfAFP1 or AlfAFP2 to allow expression of antifungally effective amounts
CC   of the polypeptide. Such transformed plants may be e.g. apple, wheat,
CC   cotton and especially potato. Micro-organisms may also be transformed
CC   to produce the polypeptides, and applied to plants to control plant
CC   fungi. The polypeptides can also be included with a suitable solvent in
CC   antifungal compositions and these can be administered to plants to
CC   control plant fungi. Such compositions and genetically engineered plants
CC   may also contain additional molecules e.g. the compositions can contain
CC   other antifungal agents or the plants contain DNA encoding insecticidal
CC   (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC   to prepare antibodies useful to detect polypeptides or isolate other
CC   alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC   to produce polypeptides and transgenic plants and as probes or primers in
CC   nucleic acid hybridisation e.g. to detect complementary sequences in
CC   samples, and to prepare mutants or isolate similar sequences from related
CC   species.
XX
SQ   Sequence 293 BP; 82 A; 60 C; 72 G; 77 T; 2 other;

  Query Match          62.8%;  Score 86.6;  DB 19;  Length 293;
  Best Local Similarity   83.1%;  Pred. No. 4e-21;
  Matches   98;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
          || |||||||||||||  | | ||| ||||||||||||||  ||||||||||  ||||
Db    176 ACTTGTGAGAATTTGGCTAACACATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCAC 235

Qy     64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 121
          ||||  |||||||||  ||  | |||| || ||||| ||||||||||||||||||||| |
Db    236 TGCAAAACCAAAGAACACTTACTTAGCGGNAGGTGCAGGGACGACTTCCGCTGCTGCT 293


RESULT 8
AAD17530
ID   AAD17530 standard; cDNA; 494 BP.
XX
AC   AAD17530;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Soybean Gly m2 protein encoding cDNA from clone sls1c.pk027.a11.
XX
KW   Soybean; allergen; transgenic plant; P34 protein; Gly m Bd 30K; Gly m 1;
KW   soybean vacuolar protein; Gly m IA; Gly m IB; rGLY m3; Glycinin G1;
KW   alaB1b; food; infant formula; animal feed; coating; salad oil; syrup;
KW   spraying oil; roasting oil; frying oil; cracker; confectionery product;
KW   snack food; topping; sauce; batter; breading mixture; baking mix; dough;
KW   Gly m2 protein; clone sls1c.pk027.a11; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..273
FT                   /*tag=  a
FT                   /product= "Soybean Gly m2 protein"
XX
PN   WO200168887-A2.
XX
PD   20-SEP-2001.
XX
PF   15-MAR-2001; 2001WO-US08254.
XX
PR   16-MAR-2000; 2000US-0189823.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Jung R,  Kinney AJ;
XX
DR   WPI; 2001-582460/65.
DR   P-PSDB; AAE10361.
XX
PT   Recombinant expression construct to lower allergen (e.g. Gly m Bd 30K)
PT   content of a soybean, comprises a nucleic acid fragment encoding the
PT   allergen, useful for producing soybean plants which can be used to make
PT   soybean products
XX
PS   Example 7; Page 51-52; 57pp; English.
XX
CC   The patent discloses hypoallergenic transgenic soybeans and recombinant
CC   expression constructs to lower soybean vacuolar protein, commonly known
CC   as P34 (Gly m Bd 30K or Gly m 1) and other allergens such as Gly m IA,
CC   Gly m IB, rGLY m3 or Glycinin G1 (alaB1b). The allergen content of the
CC   soybean is reduced by sense suppression which is accomplished by using
CC   the expression construct that comprises a nucleic acid fragment encoding
CC   the allergen. The constructs are useful for producing hypoallergenic
CC   transgenic soybean plants which can be used to make hypoallergenic
CC   soybean products which can be used in a variety of food (e.g. infant
CC   formulas) and animal feed applications. The oil made from seeds of the
CC   hypoallergenic transgenic soybean plants can be used as ingredients,
CC   as coatings, as salad oils, as spraying oils, as roasting oils, and
CC   as frying oils. The foods in which the oil may be used include crackers
CC   and snack foods, confectionery products, syrups and toppings, sauces,
CC   batter and breading mixtures, baking mixes and doughs. The present
CC   sequence is soybean Gly m2 protein encoding cDNA from sls1c.pk027.a11
CC   clone. This sequence is a minor soybean seed allergen.
XX
SQ   Sequence 494 BP; 153 A; 97 C; 103 G; 134 T; 7 other;

  Query Match          44.5%;  Score 61.4;  DB 22;  Length 494;
  Best Local Similarity   70.2%;  Pred. No. 5.4e-12;
  Matches   99;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;
```

```
Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || || |||||  |||| |||| ||| ||||| ||||||||      | |  | || ||
Db     133 ACTTGCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGAT 192

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             ||||||||  | |||||||  ||    | || || || || |||||||| || |||||
Db     193 GATCACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGT 252

Qy     118 TGGTGTACTAAAAGATGTTAA 138
           ||||| || ||||  ||||||
Db     253 TGGTGCACCAAAAACTGTTAA 273
```

RESULT 9
AAQ70126
ID AAQ70126 standard; cDNA; 141 BP.
XX
AC AAQ70126;
XX
DT 14-FEB-1995 (first entry)
XX
DE Antimicrobial Lc-AFP.
XX
KW Antimicrobial; Lc-AFP; symbiosis; disease-resistance;
KW fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc;
KW crop improvement; endophyte; ss.
XX
OS Lathyrus cicerca.
XX
PN WO9416076-A.
XX
PD 21-JUL-1994.
XX
PF 05-JAN-1994; 94WO-GB00012.
XX
PR 08-JAN-1993; 93GB-0000281.
XX
PA (ZENE) ZENECA LTD.
XX
PI Dubock AC, Powell KA, Rees SB;
XX
DR WPI; 1994-249223/30.
DR P-PSDB; AAR57322.
XX
PT Antimicrobial protein producing endo-symbiotic microorganisms -
PT is produced by combining nucleic acids encoding the protein with
PT an endophyte, useful for protecting plant hosts from esp. fungal
PT disease
XX
PS Disclosure; Page 30; 39pp; English.
XX
CC Plant-derived antimicrobial proteins are expressed in endosymbiotic
CC Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated
CC with recombinant Cxc are protected against fungal disease. A
CC suitable antimicrobial protein is Lc-AFP from L. cicerca. A
CC possible predicted sequence for the Lc-AFP gene is given in AAQ70126.
XX
SQ Sequence 141 BP; 43 A; 30 C; 32 G; 33 T; 3 other;

Query Match 29.0%; Score 40; DB 15; Length 141;
Best Local Similarity 60.6%; Pred. No. 0.00017;
Matches 83; Conservative 0; Mismatches 48; Indels 6; Gaps 1;

```
Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  |  | |||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
```

```
Db     124 TGGTGCACTAGAAACTG 140
```

RESULT 10
AAV39197/c
ID AAV39197 standard; DNA; 47 BP.
XX
AC AAV39197;
XX
DT 25-SEP-1998 (first entry)
XX
DE Antifungal polypeptide AlfAFP2 3' gene specific primer.
XX
KW Antifungal polypeptide; alfalfa plant; Medicago; fungal resistance;
KW plant pathogenic fungus; AlfAFP1; AlfAFP2; PCR primer; ss.
XX
OS Synthetic.
OS Medicago sativa.
XX
PN WO9826083-A1.
XX
PD 18-JUN-1998.
XX
PF 11-DEC-1997; 97WO-US22662.
XX
PR 13-DEC-1996; 96US-0766355.
XX
PA (MONS) MONSANTO CO.
XX
PI Hakimi S, Liang J, Rosenberger CA, Shah DM, Wu YS;
XX
DR WPI; 1998-348537/30.
XX
PT Antifungal poly:peptide(s) and genes isolated from alfalfa plant(s)
PT - used to control plant pathogenic fungi and to produce transformed
PT plants with increased fungal resistance
XX
PS Example 4; Page 78; 97pp; English.
XX
CC This primer is used for the PCR amplification of the cDNA encoding an
CC antifungal polypeptide, AlfAFP2. The antifungal polypeptides AlfAFP1 and
CC AlfAFP2 isolated from alfalfa plants (Medicago) are useful to control
CC plant fungi, especially pathogenic fung, by transforming plant cells
CC with a vector comprising sequences encoding AlfAFP1 or AlfAFP2 to allow
CC expression of antifungally effective amounts of the polypeptide. Such
CC transformed plants may be e.g. apple, wheat, cotton and especially
CC potato. Micro-organisms may also be transformed to produce the
CC polypeptides, and applied to plants to control plant fungi. The
CC polypeptides can also be included with a suitable solvent in antifungal
CC compositions and these can be administered to plants to control plant
CC fungi. Such compositions and genetically engineered plants may also
CC contain additional molecules e.g. the compositions can contain other
CC antifungal agents or the plants contain DNA encoding insecticidal
CC (e.g. Bacillus thuringiensis) proteins. The polypeptides are also useful
CC to prepare antibodies useful to detect polypeptides or isolate other
CC alfalfa plant antifungal protein antigens. The nucleic acids are useful
CC to produce polypeptides and transgenic plants and as probes or primers in
CC nucleic acid hybridisation e.g. to detect complementary sequences in
CC samples, and to prepare mutants or isolate similar sequences from related
CC species.
XX
SQ Sequence 47 BP; 11 A; 13 C; 11 G; 12 T; 0 other;

Query Match 28.3%; Score 39; DB 19; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy     100 AGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 138
           |||||||||||||||||||||||||||||||||||||||
Db      47 AGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 9
```

RESULT 11

```
AAQ38648
ID   AAQ38648 standard; DNA; 138 BP.
XX
AC   AAQ38648;
XX
DT   07-JUL-1993  (first entry)
XX
DE   Encodes antifungal protein Lc-AFP1.
XX
KW   Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;
KW   fungicide; bacteriocide; antibiotic; antifungal; gram positive;
KW   plant disease resistance; low toxicity.
XX
OS   Lathyrus cicera.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..138
FT                   /*tag=  a
XX
PN   WO9305153-A.
XX
PD   18-MAR-1993.
XX
PF   27-AUG-1992;    92WO-GB01570.
XX
PR   29-AUG-1991;    91GB-0018523.
PR   13-FEB-1992;    92GB-0003038.
PR   25-JUN-1992;    92GB-0013526.
XX
PA   (ICIL ) IMPERIAL CHEM IND PLC.
XX
PI   Broekaert WF,  Cammue BPA,  Osborn RW,  Rees SB,  Terras FRG;
PI   Vanderleyden J;
XX
DR   WPI; 1993-100978/12.
XX
PT   Biocidal proteins isolated from seeds of plants - e.g. brassica
PT   or dahlia, useful for increasing plants' resistance to fungal and
PT   bacterial diseases
XX
PS   Disclosure; Fig 31A; 110pp; English.
XX
CC   This sequence appears to encode antifungal protein Lc-AFP1 from
CC   Lathyrus cicera - see AAR33760. The exact source and isolation of the
CC   sequence is unclear from the specification.
XX
SQ   Sequence 138 BP; 43 A; 30 C; 32 G; 33 T; 0 other;

  Query Match            23.3%;  Score 32.2;  DB 14;  Length 138;
  Best Local Similarity   58.8%;  Pred. No. 0.11;
  Matches   77;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  |  | ||||||||||| ||  | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || ||| ||||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCTGCTGG 123

Qy     118 TGGTGTACTAA 128
           ||   ||  ||
Db     124 TGCACTAGAAA 134


RESULT 12
AAZ06831/c
ID   AAZ06831 standard; DNA; 37948 BP.
XX
AC   AAZ06831;
XX
DT   09-NOV-1999  (first entry)
XX
DE   Photorhabdus luminescens 38kb DNA fragment.
XX
KW   Symbiotic bacterium; nematode; insect; larva; toxin;
KW   insecticide; ds.
XX
OS   Photorhabdus luminescens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1898
FT                   /*tag=  a
FT                   /partial
FT                   /label= orf7
FT   CDS             2416..9909
FT                   /*tag=  b
FT                   /label= hph3
FT   CDS             complement (2817..3395)
FT                   /*tag=  c
FT                   /label= orf18
FT   CDS             9966..14633
FT                   /*tag=  d
FT                   /label= orf4
FT   CDS             14699..15007
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FT                   /label= orf19
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FT                   /label= orf5
FT                   /product= "Insecticidal toxin"
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FT                   /label= orf22
FT   CDS             complement (18235..19167)
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FT                   /label= orf10
FT   CDS             complement (19385..20116)
FT                   /*tag=  i
FT                   /label= orf14
FT   CDS             complement (20217..20963)
FT                   /*tag=  j
FT                   /label= orf13
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FT                   /label= orf11
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FT                   /*tag=  l
FT                   /label= hph2
FT                   /product= "Insecticidal toxin"
FT   CDS             31393..35838
FT                   /*tag=  m
FT                   /label= orf2
FT                   /product= "Insecticidal toxin"
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FT                   /label= orf21
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FT                   /*tag=  o
FT                   /label= orf16
FT   CDS             complement (36654..37781)
FT                   /*tag=  p
FT                   /label= orf8
XX
PN   WO9942589-A2.
XX
PD   26-AUG-1999.
XX
PF   18-FEB-1999;    99WO-EP01015.
XX
PR   20-JAN-1999;    99US-0116439.
PR   20-FEB-1998;    98US-0027080.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
```

PI Anderson AR, Chen JS, Dunn MM, Hart HP, Kramer VC;
PI Morgan MK, Warren GW;
XX
DR WPI; 1999-527479/44.
DR P-PSDB; AAY33728, AAY33729, AAY33730.
XX
PT New nucleic acid from Photorhabdus luminescens encoding insecticidal
PT toxins, used for making resistant transgenic plants
XX
PS Claim 1; Page 99-130; 148pp; English.
XX
CC This sequence represents an approximately 38kb fragment of Photorhabdus
CC luminescens DNA comprised in the plasmid pNOV2400 (NRRL B-30077).
CC This sequence contains 16 open reading frames (orfs) which encode
CC three insecticidal toxins. This sequence was isolated from a
CC P. luminescens cosmid library which had been screened for
CC insecticidal activity. P. luminescens is a member of the
CC Enterobacteriaceae family and is a symbiotic bacterium of nematodes
CC of the genus Heterorhabditis. The nematodes colonise insect larvae, kill
CC them, and their offspring feed on the dead larvae. However, the
CC insecticidal agents are produced by P. luminescens rather than the
CC nematodes. The toxins have activity against Lepidopteran insects such as
CC Cabbage Looper (Trichoplusia ni), European Corn Borer (Ostrinia nubialis)
CC and Fall Armyworm (Spodoptera frugiperda) and also against Coleopteran
CC insects (e.g., Colorado Potato Beetle, Leptinotarsa decimlineata). In
CC addition the toxins are active against strains resistant to known
CC insecticides. This sequence can be used to generate transgenic plants of
CC various species that are resistant to economically important insect pests
CC and also for recombinant production of toxins for use as insecticides.
XX
SQ Sequence 37948 BP; 11822 A; 8637 C; 7661 G; 9828 T; 0 other;

Query Match 22.0%; Score 30.4; DB 20; Length 37948;
Best Local Similarity 57.3%; Pred. No. 3.5;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 31 AGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGT 90
Db 14516 ACGGAACCAGCCTTTTGCGGTAGTGACCTTGATTTCTCGACCAATGGGATCATAGACATG 14457

Qy 91 GGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACT 126
Db 14456 GGTATCTGCATAGGCTTCTTCTGTCCGCCGGGCACT 14421

RESULT 13
AAS62653/c
ID AAS62653 standard; cDNA; 2172 BP.
XX
AC AAS62653;
XX
DT 14-FEB-2002 (first entry)
XX
DE cDNA sequence #440 encoding novel human secreted protein.
XX
KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW immunosuppressive; antirheumatic; ss.
XX
OS Homo sapiens.
XX
PN WO200177291-A2.
XX
PD 18-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-US10485.
XX
PR 06-APR-2000; 2000US-195604P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI Gulukota K, Graham JR;
XX
DR WPI; 2002-010900/01.
XX
PT New polynucleotides encoding secreted proteins useful for treating e.g.
PT asthma, HIV and Crohn's disease -
XX
PS Claim 1; Page 306; 391pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC The polynucleotide sequences of the invention are also useful in gene
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC invention that encode for novel human secreted proteins.
XX
SQ Sequence 2172 BP; 464 A; 606 C; 545 G; 557 T; 0 other;

Query Match 21.7%; Score 30; DB 24; Length 2172;
Best Local Similarity 64.3%; Pred. No. 1.7;
Matches 45; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 35 GACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAA 94
Db 1769 GACCCACATTTAAATGAGCTGACAGTCCCAGCAGGACTACAGAGGAACCAGTTAGGGGAA 1710

Qy 95 GGTGTAGGGA 104
Db 1709 GCTGCCAGGA 1700

RESULT 14
AAT24882/c
ID AAT24882 standard; cDNA to mRNA; 276 BP.
XX
AC AAT24882;
XX
DT 05-NOV-1996 (first entry)
XX
DE Human gene signature HUMGS06988.
XX
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX
OS Homo sapiens.
XX
PN WO9514772-A1.
XX
PD 01-JUN-1995.
XX
PF 11-NOV-1994; 94WO-JP01916.
XX
PR 12-NOV-1993; 93JP-0355504.
XX
PA (MATS/) MATSUBARA K.
PA (OKUB/) OKUBO K.
XX
PI Matsubara K, Okubo K;
XX
DR WPI; 1995-206931/27.
XX
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.

```
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 1718; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in AAT19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 276 BP; 85 A; 50 C; 61 G; 66 T; 14 other;

  Query Match             21.0%;  Score 29;  DB 16;  Length 276;
  Best Local Similarity   55.2%;  Pred. No. 1.9;
  Matches   53;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy       3 AACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCA 62
           || || |   || ||    |  ||||| | || |      |||  |  || | |||  ||
Db     218 AATATNTCTTAACTTCTGGGGNAAATACATGGTANTGCCATTTCTTAATTATCACAGACA 159

Qy      63 CTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTG 98
           |||  ||    |||   || | |||| || | || ||
Db     158 CTGAACTCAAAAATTAAAGGAAGTTCGTTGCAGATG 123


RESULT 15
AAS62577
ID   AAS62577 standard; cDNA; 1937 BP.
XX
AC   AAS62577;
XX
DT   14-FEB-2002  (first entry)
XX
DE   cDNA sequence #364 encoding novel human secreted protein.
XX
KW   Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW   immune deficiency disorder; blood disorder; inflammatory disorder;
KW   infectious disorder; gene therapy; antimicrobial; hepatotropic;
KW   immunosuppressive; antirheumatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200177291-A2.
XX
PD   18-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-US10485.
XX
PR   06-APR-2000; 2000US-195604P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Wong GG,  Clark HF,  Fechtel K,  Agostino MJ,  Howes SH,  Resnick RJ;
PI   Gulukota K,  Graham JR;
XX
DR   WPI; 2002-010900/01.
XX
PT   New polynucleotides encoding secreted proteins useful for treating e.g.
PT   asthma, HIV and Crohn's disease -
XX
PS   Claim 1; Page 267; 391pp; English.
XX
CC   The present invention relates to the isolation of novel cDNA sequences
CC   which encode human secreted proteins. The cDNA sequences have been
CC   derived from a variety of human tissues. The invention also provides
CC   a method for producing proteins from these polynucleotide sequences.
CC   The proteins are useful for identifying compounds that modulate their
CC   activity and production, and the cell is also useful for identifying
CC   compounds that modulate expression of the polynucleotide sequences
CC   encoding the secreted proteins. The sequences of the invention are
CC   useful for treating diseases such as hyperproliferative disorders
CC   (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC   immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC   sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC   disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC   The polynucleotide sequences of the invention are also useful in gene
CC   therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC   invention that encode for novel human secreted proteins.
XX
SQ   Sequence 1937 BP; 613 A; 304 C; 309 G; 711 T; 0 other;

  Query Match             21.0%;  Score 29;  DB 24;  Length 1937;
  Best Local Similarity   57.0%;  Pred. No. 3.8;
  Matches   53;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy      15 TTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAA 74
           ||||  | |  | |  ||||    |||.|  || |   |  |   || ||||| ||  |
Db     891 TTTGTTAAAATAGTGAAGGGACAAATGTTAAAGGGTAAGATAATTTCCCTGCAAAAGGAC 950

Qy      75 AGAGAACGCAGTTAGTGGAAGGTGTAGGGACGA 107
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Db     951 ACAGAAGGCAGTCTTAAGAAGATGAATGGATGA 983


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Job time : 84.9108 secs
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GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

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Sequence: 1 AGAACATGTGAGAATTTGGC.....GGTGTACTAAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	138	100.0	250	3	US-08-766-355-13	Sequence 13, Appl
	2	138	100.0	250	4	US-09-003-198A-13	Sequence 13, Appl
	3	138	100.0	250	4	US-09-428-805-13	Sequence 13, Appl
	4	138	100.0	490	4	US-09-003-198A-19	Sequence 19, Appl
	5	138	100.0	507	3	US-08-766-355-10	Sequence 10, Appl
	6	138	100.0	507	4	US-09-003-198A-10	Sequence 10, Appl
	7	138	100.0	507	4	US-09-428-805-10	Sequence 10, Appl
	8	120.8	87.5	189	4	US-09-003-198A-18	Sequence 18, Appl
	9	119.4	86.5	200	3	US-08-766-355-5	Sequence 5, Appli
	10	119.4	86.5	200	4	US-09-003-198A-5	Sequence 5, Appli
	11	119.4	86.5	200	4	US-09-428-805-5	Sequence 5, Appli
	12	117.8	85.4	327	3	US-08-766-355-9	Sequence 9, Appli
	13	117.8	85.4	327	4	US-09-003-198A-9	Sequence 9, Appli
	14	117.8	85.4	327	4	US-09-428-805-9	Sequence 9, Appli
	15	86.6	62.8	293	3	US-08-766-355-6	Sequence 6, Appli
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	18	40	29.0	141	1	US-08-377-687-35	Sequence 35, Appl
	19	40	29.0	141	1	US-08-777-192-35	Sequence 35, Appl
	20	40	29.0	141	4	US-08-971-982-35	Sequence 35, Appl
c	21	39	28.3	47	3	US-08-766-355-12	Sequence 12, Appl
c	22	39	28.3	47	4	US-09-003-198A-12	Sequence 12, Appl
c	23	39	28.3	47	4	US-09-428-805-12	Sequence 12, Appl
c	24	30.4	22.0	37948	4	US-09-251-645-11	Sequence 11, Appl
	25	28.6	20.7	1400	3	US-09-191-099-7	Sequence 7, Appli
	26	28.6	20.7	1446	3	US-09-191-099-8	Sequence 8, Appli
c	27	28.2	20.4	2997	3	US-08-486-343A-3	Sequence 3, Appli
c	28	28.2	20.4	2997	5	PCT-US95-07349-3	Sequence 3, Appli
c	29	27.6	20.0	1231	4	US-09-015-188-5	Sequence 5, Appli
	30	25.8	18.7	1212	2	US-09-092-770-18	Sequence 18, Appl
	31	25.8	18.7	1212	4	US-09-222-851-18	Sequence 18, Appl
	32	25.8	18.7	1215	2	US-09-092-770-8	Sequence 8, Appli
	33	25.8	18.7	1215	4	US-09-222-851-8	Sequence 8, Appli
	34	25.4	18.4	1366	3	US-09-191-099-4	Sequence 4, Appli
	35	25.4	18.4	1413	3	US-09-191-099-1	Sequence 1, Appli
	36	25.4	18.4	1462	3	US-09-191-099-3	Sequence 3, Appli
	37	25.4	18.4	1503	4	US-08-943-571-1	Sequence 1, Appli
	38	25.4	18.4	1589	4	US-09-464-483-1	Sequence 1, Appli
	39	25.4	18.4	1589	4	US-09-414-664-1	Sequence 1, Appli
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	42	25.4	18.4	3791	3	US-09-377-310-1	Sequence 1, Appli
c	43	25.4	18.4	4614	1	US-08-325-267A-1	Sequence 1, Appli
	44	25.4	18.4	15225	2	US-08-892-403A-2	Sequence 2, Appli
	45	25.4	18.4	62804	4	US-09-800-960-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-766-355-13
; Sequence 13, Application US/08766355
; Patent No. 6121436
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip Maganlal
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; APPLICANT: Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 77210.
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,355
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-766-355-13

Query Match 100.0%; Score 138; DB 3; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Db    105 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
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Db    165 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 224

Qy    121 TGTACTAAAAGATGTTAA 138
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Db    225 TGTACTAAAAGATGTTAA 242


RESULT 2
US-09-003-198A-13
; Sequence 13, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-003-198A-13

  Query Match             100.0%;  Score 138;  DB 4;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 224

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    225 TGTACTAAAAGATGTTAA 242


RESULT 3
US-09-428-805-13
; Sequence 13, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-428-805-13

  Query Match             100.0%;  Score 138;  DB 4;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 164

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 224

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    225 TGTACTAAAAGATGTTAA 242


RESULT 4
US-09-003-198A-19
; Sequence 19, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
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;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  490 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-003-198A-19

  Query Match             100.0%;  Score 138;  DB 4;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 215

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 275

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    276 TGTACTAAAAGATGTTAA 293


RESULT 5
US-08-766-355-10
; Sequence 10, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  507 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 424, 485)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-10

  Query Match             100.0%;  Score 138;  DB 3;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 232

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 292

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    293 TGTACTAAAAGATGTTAA 310


RESULT 6
US-09-003-198A-10
; Sequence 10, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  507 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 424, 485)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-10

  Query Match             100.0%;  Score 138;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 232

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 292

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    293 TGTACTAAAAGATGTTAA 310


RESULT 7
US-09-428-805-10
; Sequence 10, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  507 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(17, 424, 485)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-10

  Query Match             100.0%;  Score 138;  DB 4;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-42;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 232

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 292

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    293 TGTACTAAAAGATGTTAA 310


RESULT 8
US-09-003-198A-18
; Sequence 18, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  189 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
US-09-003-198A-18

  Query Match             87.5%;  Score 120.8;  DB 4;  Length 189;
  Best Local Similarity   98.4%;  Pred. No. 3.9e-36;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
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Db     63 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 122

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 182

Qy    121 TGTA 124
          || |
Db    183 TGGA 186


RESULT 9
US-08-766-355-5
; Sequence 5, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  17
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-5

  Query Match             86.5%;  Score 119.4;  DB 3;  Length 200;
  Best Local Similarity   99.2%;  Pred. No. 1.3e-35;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 139

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 199

Qy    121 T 121
          |
Db    200 T 200


RESULT 10
US-09-003-198A-5
; Sequence 5, Application US/09003198A
; Patent No. 6316407
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  17
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-5

  Query Match             86.5%;  Score 119.4;  DB 4;  Length 200;
  Best Local Similarity   99.2%;  Pred. No. 1.3e-35;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 139

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    140 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 199

Qy    121 T 121
          |
Db    200 T 200


RESULT 11
US-09-428-805-5
; Sequence 5, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  200 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  17
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-5

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  Best Local Similarity   99.2%;  Pred. No. 1.3e-35;
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Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
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Qy    121 T 121
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Db    200 T 200


RESULT 12
US-08-766-355-9
; Sequence 9, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/766,355
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-9

  Query Match             85.4%;  Score 117.8;  DB 3;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 6.6e-35;
  Matches  122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy     10 GAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 69
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Db      1 GAGAATTTGGCGGATAAGTATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 60

Qy     70 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 129
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Db     61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy    130 AGATGTTAA 138
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Db    121 AGATGTTAA 129


RESULT 13
US-09-003-198A-9
; Sequence 9, Application US/09003198A
; Patent No. 6316407
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;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/003,198A
;      FILING DATE:  07-JAN-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Patterson, Melinda L.
;      REGISTRATION NUMBER:  33,062
;      REFERENCE/DOCKET NUMBER:  MOBT:193
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (713) 787-1400
;      TELEFAX:  (713) 787-1440
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-003-198A-9

  Query Match             85.4%;  Score 117.8;  DB 4;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 6.6e-35;
  Matches  122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      10 GAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 69
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Qy      70 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 129
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Db      61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy     130 AGATGTTAA 138
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Db     121 AGATGTTAA 129


RESULT 14
US-09-428-805-9
; Sequence 9, Application US/09428805
; Patent No. 6329504
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 77210
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  United States of America
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/428,805
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/766,355
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kitchell, Barbara S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  MOBT:063
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (512) 474-7577
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  327 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  modified_base
;      LOCATION:  one-of(244, 305)
;      OTHER INFORMATION:  /mod_base= OTHER
;      OTHER INFORMATION:  /note= "N = A or C or G or T"
US-09-428-805-9

  Query Match             85.4%;  Score 117.8;  DB 4;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 6.6e-35;
  Matches  122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Db       1 GAGAATTTGGCGGATAAGTATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 60

Qy      70 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 129
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Db      61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy     130 AGATGTTAA 138
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Db     121 AGATGTTAA 129


RESULT 15
US-08-766-355-6
; Sequence 6, Application US/08766355
; Patent No. 6121436
;  GENERAL INFORMATION:
;    APPLICANT:  Liang, Jihong
;    APPLICANT:  Shah, Dilip Maganlal
;    APPLICANT:  Wu, Yonnie S.
;    APPLICANT:  Rosenberger, Cindy A.
;    APPLICANT:  Hakimi, Salim
;    TITLE OF INVENTION:  Antifungal Polypeptide and Methods for
;    TITLE OF INVENTION:  Controlling Plant Pathogenic Fungi
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
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;       STREET:  P.O. Box 77210
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  United States of America
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/766,355
;       FILING DATE:  Concurrently Herewith
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kitchell, Barbara S.
;       REGISTRATION NUMBER:  33,928
;       REFERENCE/DOCKET NUMBER:  MOBT:063
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (512) 474-7577
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  293 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  modified_base
;       LOCATION:  one-of(17, 265)
;       OTHER INFORMATION:  /mod_base= OTHER
;       OTHER INFORMATION:  /note= "N = A or C or G or T"
US-08-766-355-6

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Db     176 ACTTGTGAGAATTTGGCTAACACATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCAC 235

Qy      64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 121
           |||| |||||||||  ||  | |||| || ||||| ||||||||||||||||||||| |
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Title: US-10-010-731-13_COPY_105_242
Perfect score: 138
Sequence: 1 AGAACATGTGAGAATTTGGC.....GGTGTACTAAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	138	100.0	250	9	US-10-010-731-13	Sequence 13, Appl
	2	138	100.0	490	9	US-10-010-731-19	Sequence 19, Appl
	3	138	100.0	507	9	US-10-010-731-10	Sequence 10, Appl
	4	120.8	87.5	189	9	US-10-010-731-18	Sequence 18, Appl
	5	119.4	86.5	200	9	US-10-010-731-5	Sequence 5, Appli
	6	117.8	85.4	327	9	US-10-010-731-9	Sequence 9, Appli
	7	86.6	62.8	293	9	US-10-010-731-6	Sequence 6, Appli
	8	64.8	47.0	420	9	US-10-178-213-436	Sequence 436, App
	9	64.4	46.7	563	9	US-10-178-213-439	Sequence 439, App
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	12	43.6	31.6	464	9	US-10-178-213-379	Sequence 379, App
	13	40	29.0	141	10	US-09-759-584-35	Sequence 35, Appl
c	14	39	28.3	47	9	US-10-010-731-12	Sequence 12, Appl
c	15	30.2	21.9	463	9	US-09-918-995-11517	Sequence 11517, A
c	16	30	21.7	2172	10	US-09-822-830A-440	Sequence 440, App
	17	29	21.0	1937	10	US-09-822-830A-364	Sequence 364, App
	18	28.8	20.9	15109	7	US-08-781-986A-44	Sequence 44, Appl
	19	28.6	20.7	1544	10	US-09-726-774-10	Sequence 10, Appl
c	20	28	20.3	1503841	9	US-09-946-807-1	Sequence 1, Appli
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	26	26.8	19.4	333	9	US-09-535-459-1813	Sequence 1813, Ap
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	28	26.8	19.4	449	10	US-09-764-847-328	Sequence 328, App
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c	32	26.4	19.1	393	9	US-10-040-862-8003	Sequence 8003, Ap
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c	39	26.2	19.0	1661	9	US-09-764-891-2554	Sequence 2554, Ap
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	44	26	18.8	426	9	US-09-849-626-913	Sequence 913, App
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ALIGNMENTS

RESULT 1
US-10-010-731-13
; Sequence 13, Application US/10010731
; Publication No. US20030041347A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip Maganlal
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; Hakimi, Salim
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/010,731
; FILING DATE: 13-No. US20030041347A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/003,198
; FILING DATE: 07-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 base pairs

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;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-010-731-13

  Query Match            100.0%;  Score 138;  DB 9;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-38;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
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RESULT 2
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; Sequence 19, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;         APPLICANT: Liang, Jihong
;                    Shah, Dilip Maganlal
;                    Wu, Yonnie S.
;                    Rosenberger, Cindy A.
;                    Hakimi, Salim
;         TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                             Controlling Plant Pathogenic Fungi
;         NUMBER OF SEQUENCES: 19
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Arnold White & Durkee
;              STREET: P.O. Box 4433
;              CITY: Houston
;              STATE: Texas
;              COUNTRY: USA
;              ZIP: 77210
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/010,731
;              FILING DATE: 13-No. US20030041347A1-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/003,198
;              FILING DATE: 07-JAN-1998
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Patterson, Melinda L.
;              REGISTRATION NUMBER: 33,062
;              REFERENCE/DOCKET NUMBER: MOBT:193
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (713) 787-1400
;              TELEFAX: (713) 787-1440
;    INFORMATION FOR SEQ ID NO: 19:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 490 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-010-731-19

  Query Match            100.0%;  Score 138;  DB 9;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-38;
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Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 275

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    276 TGTACTAAAAGATGTTAA 293


RESULT 3
US-10-010-731-10
; Sequence 10, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;         APPLICANT: Liang, Jihong
;                    Shah, Dilip Maganlal
;                    Wu, Yonnie S.
;                    Rosenberger, Cindy A.
;                    Hakimi, Salim
;         TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                             Controlling Plant Pathogenic Fungi
;         NUMBER OF SEQUENCES: 19
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Arnold White & Durkee
;              STREET: P.O. Box 4433
;              CITY: Houston
;              STATE: Texas
;              COUNTRY: USA
;              ZIP: 77210
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/010,731
;              FILING DATE: 13-No. US20030041347A1-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/003,198
;              FILING DATE: 07-JAN-1998
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Patterson, Melinda L.
;              REGISTRATION NUMBER: 33,062
;              REFERENCE/DOCKET NUMBER: MOBT:193
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (713) 787-1400
;              TELEFAX: (713) 787-1440
;    INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 507 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         FEATURE:
;              NAME/KEY:  modified_base
;              LOCATION:  one-of(17, 424, 485)
;              OTHER INFORMATION:  /mod_base= OTHER
;              /note= "N = A or C or G or T"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-010-731-10

  Query Match            100.0%;  Score 138;  DB 9;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-38;
  Matches  138;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 232

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 292

Qy    121 TGTACTAAAAGATGTTAA 138
          ||||||||||||||||||
Db    293 TGTACTAAAAGATGTTAA 310


RESULT 4
US-10-010-731-18
; Sequence 18, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 189 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-010-731-18

  Query Match             87.5%;  Score 120.8;  DB 9;  Length 189;
  Best Local Similarity   98.4%;  Pred. No. 1.3e-32;
  Matches  122;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     63 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 122

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    123 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 182

Qy    121 TGTA 124
          ||||
Db    183 TGGA 186


RESULT 5
US-10-010-731-5
; Sequence 5, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 200 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  17
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-010-731-5

  Query Match             86.5%;  Score 119.4;  DB 9;  Length 200;
  Best Local Similarity   99.2%;  Pred. No. 4.2e-32;
  Matches  120;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     80 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACT 139

Qy     61 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    140 CACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGC 199

Qy    121 T 121
          |
Db    200 T 200
```

```
RESULT 6
US-10-010-731-9
; Sequence 9, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 327 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  one-of(244, 305)
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-010-731-9

  Query Match             85.4%;  Score 117.8;  DB 9;  Length 327;
  Best Local Similarity   94.6%;  Pred. No. 1.8e-31;
  Matches  122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      10 GAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 69
           |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 GAGAATTTGGCGGATAAGTATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACA 60

Qy      70 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTAAA 129
           |||||||||||||||||||||||||||||||||| ||||| || || | ||||||||||
Db      61 ACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGATGACTTTCGTTGTTAGTGTACTAAA 120

Qy     130 AGATGTTAA 138
           |||||||||
Db     121 AGATGTTAA 129


RESULT 7
US-10-010-731-6
; Sequence 6, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 6:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 293 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        FEATURE:
;             NAME/KEY:  modified_base
;             LOCATION:  one-of(17, 265)
;             OTHER INFORMATION:  /mod_base= OTHER
;             /note= "N = A or C or G or T"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-010-731-6

  Query Match             62.8%;  Score 86.6;  DB 9;  Length 293;
  Best Local Similarity   83.1%;  Pred. No. 1.4e-20;
  Matches   98;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
           || |||||||||||||  | | ||| ||||||||||||||  ||||||||||| ||||
Db     176 ACTTGTGAGAATTTGGCTAACACATACAGGGGACCATGCTTCGGTGGTTGTGACTTTCAC 235

Qy      64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGT 121
           |||| |||||||||  ||  | |||| || ||||| |||||||||||||||||||| |
Db     236 TGCAAAACCAAAGAACACTTACTTAGCGGNAGGTGCAGGGACGACTTCCGCTGCTGCT 293


RESULT 8
US-10-178-213-436
; Sequence 436, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
```

```
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 436
;   LENGTH: 420
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (31)...(264)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (118)...(261)
US-10-178-213-436

  Query Match             47.0%;  Score 64.8;  DB 9;  Length 420;
  Best Local Similarity   71.5%;  Pred. No. 7e-13;
  Matches  103;  Conservative    0;  Mismatches   32;  Indels    9;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGG---------TTGT 54
           |||||||||||| | ||||||| ||  ||||| ||||||||   |||          ||
Db     121 ACATGTGAGAATCTTGCAGATACATTCAGGGGTCCATGCTTCCCTGGAACCGCCAGCTGC 180

Qy      55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
             ||   |||||||| | ||||||| ||    | || |||||||| || ||||| || |||
Db     181 AACGATCACTGCAAGAACAAAGAGCACTTGCTCAGCGGAAGGTGCAGAGACGATTTTCGC 240

Qy     115 TGCTGGTGTACTAAAAGATGTTAA 138
           |||||||| || ||||  ||||||
Db     241 TGCTGGTGCACCAAAAACTGTTAA 264


RESULT 9
US-10-178-213-439
; Sequence 439, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 439
;   LENGTH: 563
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (106)...(333)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (190)...(330)
US-10-178-213-439

  Query Match             46.7%;  Score 64.4;  DB 9;  Length 563;
  Best Local Similarity   70.8%;  Pred. No. 1.1e-12;
  Matches  102;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy       1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGT 54
             || |||||||||| | ||||||| | ||| |||||||| || ||      | || | ||
Db     190 AGGACATGTGAGAGTCTGGCAGACACATACAGGGGACCCTGTTTCACAGATGGTAGCTGC 249

Qy      55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
             ||   ||||||||  | ||||||| ||  | | |||||||| || ||  | || || |||
Db     250 GATGATCACTGCAAGAACAAAGAGCACTTAATCAGTGGAAGATGCAGAAATGATTTTCGC 309

Qy     115 TGCTGGTGTACTAAAAGATGTTAA 138
           || ||||| || | ||  ||||||
Db     310 TGTTGGTGCACCAGAAACTGTTAA 333


RESULT 10
US-09-805-694B-5
; Sequence 5, Application US/09805694B
; Publication No. US20030041350A1
; GENERAL INFORMATION:
;  APPLICANT: Kinney, Anthony
;  TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
;  FILE REFERENCE: BB1432 US NA
;  CURRENT APPLICATION NUMBER: US/09/805,694B
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,823
;  PRIOR FILING DATE: 2000-03-16
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
;   LENGTH: 494
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (9)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (388)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (392)..(393)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (460)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (463)
;   OTHER INFORMATION: n = A, C, G, or T
;   NAME/KEY: unsure
;   LOCATION: (468)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-805-694B-5

  Query Match             44.5%;  Score 61.4;  DB 9;  Length 494;
  Best Local Similarity   70.2%;  Pred. No. 1.1e-11;
  Matches   99;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
             || ||  |||||  |||| |||| ||| ||||| ||||||||      | |  | || ||
Db     133 ACTTGCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGAT 192

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             ||||||||  | ||||||| ||    | || || || || |||||||| || |||||
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Db    193 GATCACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGT 252

Qy    118 TGGTGTACTAAAAGATGTTAA 138
          ||||| || ||||  ||||||
Db    253 TGGTGCACCAAAAACTGTTAA 273


RESULT 11
US-10-178-213-451
; Sequence 451, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 451
;   LENGTH: 461
;   TYPE: DNA
;   ORGANISM: Arachis hypogaea
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (44)...(271)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (128)...(268)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 305, 319, 357, 372, 400, 406, 420, 443, 452, 455
;   OTHER INFORMATION: n = A,T,C or G
US-10-178-213-451

  Query Match           41.7%;  Score 57.6;  DB 9;  Length 461;
  Best Local Similarity   68.3%;  Pred. No. 2.4e-10;
  Matches   97;  Conservative    0;  Mismatches   39;  Indels    6;  Gaps    1;

Qy      3 AACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGA 56
          ||| ||||||||  |||| ||||  || ||||||||||||||| |      |  | || ||
Db    130 AACGTGTGAGAACCTGGCGGATACCTACAGGGGACCATGCTTCACCACCGGAAGCTGCGA 189

Qy     57 CACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTG 116
          |   |||||||  | ||| ||| ||    | || ||  | ||  | ||||| ||||||||
Db    190 CGACCACTGCAAGAACAAGGAGCACCTGCTCAGCGGCCGCTGCCGCGACGATTTCCGCTG 249

Qy    117 CTGGTGTACTAAAAGATGTTAA 138
          ||||| || | ||  ||||||
Db    250 TTGGTGCACCAGAAACTGTTAA 271


RESULT 12
US-10-178-213-379
; Sequence 379, Application US/10178213
; Publication No. US20030041348A1
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  APPLICANT:  Navarro Acevedo, Pedro A.
;  APPLICANT:  Harvell, Leslie
;  APPLICANT:  Cahoon, Rebecca
;  APPLICANT:  McCutchen, Billy Fred
;  APPLICANT:  Lu, Albert
;  APPLICANT:  Herrmann, Rafael
;  APPLICANT:  Wong, James
;  TITLE OF INVENTION: Defensin Polynucleotides and Methods of
;  TITLE OF INVENTION:  Use
;  FILE REFERENCE: 35718/246703
;  CURRENT APPLICATION NUMBER: US/10/178,213
;  CURRENT FILING DATE:  2002-06-21
;  PRIOR APPLICATION NUMBER: 60/300,152
;  PRIOR FILING DATE: 2001-06-22
;  PRIOR APPLICATION NUMBER: 60/300,241
;  PRIOR FILING DATE: 2001-06-22
;  NUMBER OF SEQ ID NOS: 469
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 379
;   LENGTH: 464
;   TYPE: DNA
;   ORGANISM: Cyamopsis tetragonoloba
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (32)...(256)
;   FEATURE:
;   NAME/KEY: mat_peptide
;   LOCATION: (116)...(253)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2
;   OTHER INFORMATION: n = A,T,C or G
US-10-178-213-379

  Query Match           31.6%;  Score 43.6;  DB 9;  Length 464;
  Best Local Similarity   66.7%;  Pred. No. 1.9e-05;
  Matches   96;  Conservative    0;  Mismatches   39;  Indels    9;  Gaps    2;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGT 54
          |||||||||||| |  |||||| | ||| |||||||| || || |      || | ||
Db    116 AGAACATGTGAGAGTCCGGCAGACACATACAGGGGACCCTGTTTCACTGAGGGTAGCTGC 175

Qy     55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
          ||   ||| |||| |  ||||||  ||  | | |||||||  || |   |  | ||   |
Db    176 GATGATCATTGCAAGAACAAAGAACACTTAATCAGTGGAACATGCA---AACAGTTAGCC 232

Qy    115 TGCTGGTGTACTAAAAGATGTTAA 138
          |||||||| || | ||  ||||||
Db    233 TGCTGGTGCACCAGAAACTGTTAA 256


RESULT 13
US-09-759-584-35
; Sequence 35, Application US/09759584
; Patent No. US20010014732A1
;  GENERAL INFORMATION:
;    APPLICANT:  BROEKAERT, WILLEM F.
;    APPLICANT:  CAMMUE, BRUNO P.A.
;    APPLICANT:  OSBORN, RUPERT W.
;    APPLICANT:  REES, SARAH B.
;    APPLICANT:  TERRAS, FRANKY R.G.
;    APPLICANT:  VANDERLEYDEN, JOZEF
;    TITLE OF INVENTION:  BIOCIDAL PROTEINS
;    NUMBER OF SEQUENCES:  59
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN DARBY & CUSHMAN
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/759,584
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/377,687
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOKULIS, PAUL N.
;      REGISTRATION NUMBER:  16,773
;      REFERENCE/DOCKET NUMBER:  99042/SEE.36525/US/A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3000
;      TELEFAX:  202-822-0944
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  141 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-759-584-35

  Query Match             29.0%;  Score 40;  DB 10;  Length 141;
  Best Local Similarity   60.6%;  Pred. No. 0.00021;
  Matches   83;  Conservative    0;  Mismatches   48;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGT------TGTGAC 57
           || || |||||  |  | |  |  |  | ||||||||| ||   | |      ||  ||
Db       4 ACTTGCGAGAACCTTTCTGGAACTTTCAAGGGACCATGCATTCCAGATGGAAACTGCAAC 63

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
           |  || ||||  | ||| ||| |     ||  |||||| || || || || |||   |||
Db      64 AAGCATTGCAAGAACAACGAGCATCTTCTTTCTGGAAGATGCAGAGATGATTTCNNNTGC 123

Qy     118 TGGTGTACTAAAAGATG 134
           ||||| |||| ||  ||
Db     124 TGGTGCACTAGAAACTG 140


RESULT 14
US-10-010-731-12/c
; Sequence 12, Application US/10010731
; Publication No. US20030041347A1
;   GENERAL INFORMATION:
;        APPLICANT: Liang, Jihong
;                   Shah, Dilip Maganlal
;                   Wu, Yonnie S.
;                   Rosenberger, Cindy A.
;                   Hakimi, Salim
;        TITLE OF INVENTION: Antifungal Polypeptide and Methods for
;                            Controlling Plant Pathogenic Fungi
;        NUMBER OF SEQUENCES: 19
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Arnold White & Durkee
;             STREET: P.O. Box 4433
;             CITY: Houston
;             STATE: Texas
;             COUNTRY: USA
;             ZIP: 77210
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/010,731
;             FILING DATE: 13-No. US20030041347A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/003,198
;             FILING DATE: 07-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Patterson, Melinda L.
;             REGISTRATION NUMBER: 33,062
;             REFERENCE/DOCKET NUMBER: MOBT:193
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (713) 787-1400
;             TELEFAX: (713) 787-1440
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 47 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-010-731-12

  Query Match             28.3%;  Score 39;  DB 9;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 0.00031;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     100 AGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 138
           |||||||||||||||||||||||||||||||||||||||
Db      47 AGGGACGACTTCCGCTGCTGGTGTACTAAAAGATGTTAA 9


RESULT 15
US-09-918-995-11517/c
; Sequence 11517, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11517
;   LENGTH: 463
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(463)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-11517

  Query Match             21.9%;  Score 30.2;  DB 9;  Length 463;
  Best Local Similarity   58.2%;  Pred. No. 0.91;
  Matches   53;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy       3 AACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCA 62
           |||||| | | |     ||    | ||     | | ||  |||  ||| | ||||||  |
Db     434 AACATGGGGGGAACCTTCATGGCATTAATTTTGGCAATAATTTTTTGGATATGACACCAA 375

Qy      63 CTGCACAACCAAAGAGAACGCAGTTAGTGGA 93
           |||||| |||  ||||||||  ||   ||
Db     374 AAGCACAAGCAACAAGAACGCAAATAAATGA 344


Search completed: May  8, 2003, 07:21:33
Job time : 47.4873 secs
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GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: May 8, 2003, 05:40:33 ; Search time 500.799 Seconds
(without alignments)
4462.820 Million cell updates/sec

Title: US-10-010-731-13_COPY_105_242
Perfect score: 138
Sequence: 1 AGAACATGTGAGAATTTGGC.....GGTGTACTAAAAGATGTTAA 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	111	80.4	446	9	AJ498901	AJ498901 AJ498901
c	2	58.6	42.5	426	12	BG838678	BG838678 Gc01_03f0
	3	58.2	42.2	487	13	BI321179	BI321179 saf48d10.
	4	58	42.0	517	9	AJ308155	AJ308155 AJ308155
	5	49	35.5	366	13	BI321308	BI321308 saf50c11.
	6	43.6	31.6	574	14	BQ151477	BQ151477 NF088A06L
	7	40.8	29.6	503	12	BF633403	BF633403 NF047E03D
	8	38.6	28.0	438	13	BI642738	BI642738 TZS1161 T
c	9	35.2	25.5	686	17	AG181132	AG181132 Pan trogl
c	10	32.6	23.6	1637	12	BG247486	BG247486 602360241
c	11	31.8	23.0	542	17	AQ793341	AQ793341 HS_5439_A
c	12	31	22.5	433	17	AZ512910	AZ512910 1M0358I17
	13	30.8	22.3	567	10	BE330295	BE330295 so75h05.y
c	14	30.8	22.3	662	10	BB356735	BB356735 BB356735
	15	30.6	22.2	149	17	AZ395343	AZ395343 1M0159O08
	16	30.6	22.2	497	14	BQ119258	BQ119258 EST604834
c	17	30.4	22.0	788	10	BE560644	BE560644 601345864
c	18	30	21.7	464	17	AZ013758	AZ013758 RPCI-23-3
	19	30	21.7	1055	12	BE888496	BE888496 601512874
c	20	29.8	21.6	997	17	CNS06ZZ6	AL422968 T3 end of
	21	29.6	21.4	281	10	BB287165	BB287165 BB287165
	22	29.6	21.4	294	10	BB173276	BB173276 BB173276
c	23	29.6	21.4	299	10	BB265616	BB265616 BB265616
c	24	29.6	21.4	335	17	AZ021720	AZ021720 RPCI-23-3
c	25	29.6	21.4	342	17	AZ004823	AZ004823 RPCI-23-2
	26	29.6	21.4	805	10	BE469462	BE469462 IpHdk0184
c	27	29.6	21.4	1007	17	CNS06M2Q	AL404952 T7 end of
	28	29.4	21.3	250	9	AV113248	AV113248 AV113248
c	29	29.4	21.3	290	10	BB369954	BB369954 BB369954
c	30	29.4	21.3	442	12	BF419465	BF419465 UI-R-CA0-
	31	29.4	21.3	522	14	BQ852500	BQ852500 QGB18D04.
	32	29.4	21.3	526	14	BQ985543	BQ985543 QGE7B16.y
	33	29.4	21.3	540	14	BQ994036	BQ994036 QGF6C07.y
c	34	29.4	21.3	582	17	AZ968358	AZ968358 2M0240I08
c	35	29.4	21.3	655	17	BH120322	BH120322 RPCI-24-2
	36	29.4	21.3	813	17	AQ364702	AQ364702 nbxb0061B
c	37	29.2	21.2	331	10	BB731530	BB731530 BB731530
c	38	29.2	21.2	412	10	BB835814	BB835814 BB835814
c	39	29.2	21.2	418	10	BB833130	BB833130 BB833130
c	40	29.2	21.2	453	10	BB820106	BB820106 BB820106
c	41	29	21.0	398	9	AA582705	AA582705 nn55h06.s
	42	29	21.0	660	9	AU237466	AU237466 AU237466
c	43	29	21.0	660	13	BI101794	BI101794 602885338
	44	29	21.0	676	12	BG546289	BG546289 602573620
	45	28.8	20.9	327	9	AV090308	AV090308 AV090308

ALIGNMENTS

RESULT 1
AJ498901
LOCUS AJ498901 446 bp mRNA linear EST 09-AUG-2002
DEFINITION AJ498901 MTPOSE Medicago truncatula cDNA clone mt--acc955209h10, mRNA sequence.
ACCESSION AJ498901
VERSION AJ498901.1 GI:22089344
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 446)
AUTHORS Firnhaber,C., Bartelsmeier,V., Meyer,F., Bartels,D., Bekel,T., Linke,B., Puehler,A. and Kuester,H.
TITLE Determination of transcript sequences from developing pods including seeds of Medicago truncatula genotype A17
JOURNAL Unpublished (2002)
COMMENT Contact: Kuester H
Lehrstuhl fuer Genetik
Universitaet Bielefeld
Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES Location/Qualifiers
source 1. .446
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="mt--acc955209h10"

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                     /clone_lib="MTPOSE"
                     /tissue_type="pods including seeds"
                     /dev_stage="different stages of development"
                     /note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI;
                     genotype A17; cDNA was prepared from polyA+ enriched RNA
                     from developing pods including seeds harvested at
                     different stages of development. The cDNA was
                     directionally ligated by MediGenomix into the pGEM-T
                     vector from Promega using GCATGCGGCCGAGGCGGCCGACATG and
                     CTGCAGGCCATTATGGCCGGG adapters. Plasmids containing cDNA
                     inserts were propagated in E. coli DH10B cells."
BASE COUNT      147 a      84 c      83 g     132 t
ORIGIN

  Query Match             80.4%;  Score 111;  DB 9;  Length 446;
  Best Local Similarity   88.9%;  Pred. No. 1.5e-26;
  Matches  120;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
           || ||||||||||||||| |||||||| ||||||||||||||||||||||||| ||||||
Db     145 ACTTGTGAGAATTTGGCTGATAAATACAGGGGACCATGCTTTAGTGGTTGTGATACTCAC 204

Qy      64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
           ||||| |||||||||||| |||||||| || ||||| ||||| ||||| || || ||||||
Db     205 TGCACTACCAAAGAGAATGCAGTTAGCGGCAGGTGCAGGGATGACTTTCGTTGTTGGTGT 264

Qy     124 ACTAAAAGATGTTAA 138
           ||||||| ||||||
Db     265 ACTAAAAACTGTTAA 279


RESULT 2
BG838678/c
LOCUS       BG838678                426 bp    mRNA    linear   EST 25-MAY-2001
DEFINITION  Gc01_03f01_A Gc01_AAFC_ECORC_cold_stressed_Glycine_clandestina
            Glycine clandestina cDNA clone Gc01_03f01, mRNA sequence.
ACCESSION   BG838678
VERSION     BG838678.1  GI:14204985
KEYWORDS    EST.
SOURCE      Glycine clandestina.
  ORGANISM  Glycine clandestina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 426)
  AUTHORS   Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris
            ,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker
            ,N.A.
  TITLE     Expressed Sequence Tags from Cold-Stressed Glycine clandestina
            Seedlings
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@em.agr.ca.
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Glycine clandestina"
                     /cultivar="1035"
                     /db_xref="taxon:45687"
                     /clone="Gc01_03f01"
                     /clone_lib="Gc01_AAFC_ECORC_cold_stressed_Glycine_clandest
                     ina"
                     /tissue_type="Leaves, stem"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Plants incubated at 2 degrees under 12 hours
                     of light/day.  Harvested  after only 2-3 days of cold
                     treatment. cDNA was prepared with the  Uni-Zap cDNA kit
                     from Stratagene.  Eco RI adapters were linked followed  by
                     digest with Xho I/Eco RI and ligated to pBluescript."
BASE COUNT      116 a      92 c      86 g     125 t       7 others
ORIGIN

  Query Match             42.5%;  Score 58.6;  DB 12;  Length 426;
  Best Local Similarity   67.4%;  Pred. No. 5.5e-09;
  Matches   95;  Conservative    4;  Mismatches   36;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGTGAC 57
           || || |||||  ||||  ||| ||| ||||| ||||||||  |      |  | || ||
Db     316 ACTTGCGAGAACCTGGCTAATACATACAGGGGYCCATGCTTCACTACCGGCAGCTGCGAT 257

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             ||||||||  |  |||||  ||  | | || || ||||| ||||||:|:|| |||||:
Db     256 GATCACTGCAAGAATAAAGAACACTTACTCAGCGGCAGGTGCAGGGACVAYTTTCGCTGH 197

Qy     118 TGGTGTACTAAAAGATGTTAA 138
           |||:| || | ||  ||||||
Db     196 TGGHGCACCAGAAACTGTTAA 176


RESULT 3
BI321179
LOCUS       BI321179                487 bp    mRNA    linear   EST 29-NOV-2001
DEFINITION  saf48d10.y3 Gm-c1077 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1077-1723 5' similar to SW:10KD_VIGUN P18646 10 KD PROTEIN
            PRECURSOR ;, mRNA sequence.
ACCESSION   BI321179
VERSION     BI321179.1  GI:15000365
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 487)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Putative full length read
            vector to vector length is This clone is available through: ResGen,
            Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801
            For further information call: (800)-533-4363 or contact via email:
            ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 432.
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1077-1723"
                     /clone_lib="Gm-c1077"
                     /tissue_type="18 day old 'Williams' seedlings"
                     /dev_stage="18 day old 'Williams' seedlings"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from cotyledons of 18-day-old
                     'Williams' seedlings which were greenhouse grown in
                     potting soil. The cotyledons were flash- frozen in liquid
```

nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

```
BASE COUNT      152 a     96 c    102 g    137 t
ORIGIN

  Query Match             42.2%;  Score 58.2;  DB 13;  Length 487;
  Best Local Similarity   68.8%;  Pred. No. 8e-09;
  Matches   97;  Conservative    0;  Mismatches   38;  Indels    6;  Gaps    1;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGTGAC 57
           || || |||||  |||| |||| ||| |||||| ||||||||      | |  | || ||
Db     155 ACTTGCGAGAACCTGGCTGATACATACAGGGGTCCATGCTTCACCACTGGCAGCTGCGAT 214

Qy      58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
             |  |||||  | ||||||| ||    | || || || || |||||||| || |||||
Db     215 GATTTCTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATTTTCGCTGT 274

Qy     118 TGGTGTACTAAAAGATGTTAA 138
           ||||| || ||||  ||||||
Db     275 TGGTGCACCAAAAACTGTTAA 295


RESULT 4
AJ308155
LOCUS       AJ308155                517 bp    mRNA    linear   EST 29-OCT-2001
DEFINITION  AJ308155 SSH Pisum sativum cDNA clone PsSSH1clone91, mRNA sequence.
ACCESSION   AJ308155
VERSION     AJ308155.1  GI:16507870
KEYWORDS    EST.
SOURCE      pea.
  ORGANISM  Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
            Pisum.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Grunwald,U., Lapopin,L., Becker,A., Mann,P., Bomanskie,N.,
            Gianinazzi-Pearson,V. and Franken,P.
  TITLE     Screening for genes activated in Pisum sativum mycorrhiza by
            arbuscule development-related expression profiling
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Franken P
            Biochemistry
            Max-Planck-Institute for Terrestrial Microbiology
            Marburg, Karl-von-Frisch-Strasse, D-35043, Germany.
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Pisum sativum"
                     /cultivar="Finale"
                     /db_xref="taxon:3888"
                     /clone="PsSSH1clone91"
                     /clone_lib="SSH"
                     /tissue_type="arbuscular mycorrhiza"
                     /note="minus inoculated late mutant"
BASE COUNT      161 a     87 c    102 g    167 t
ORIGIN

  Query Match             42.0%;  Score 58;  DB 9;  Length 517;
  Best Local Similarity   68.1%;  Pred. No. 9.5e-09;
  Matches   98;  Conservative    0;  Mismatches   40;  Indels    6;  Gaps    1;

Qy       1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTT------TAGTGGTTGT 54
           | ||| |||||||||||    |  | ||  | |||||||||| |      | ||   ||
Db     159 AAAACTTGTGAGAATTTGTTTGGCACATTCAAGGGACCATGCATCCCAGATGGTAACTGC 218

Qy      55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
             |||  || ||||  | ||| ||| ||  | | ||||| ||||| ||||| || || |||
Db     219 AACAAACATTGCAGGAACAACGAGCACTTACTCAGTGGGAGGTGCAGGGATGATTTTCGC 278

Qy     115 TGCTGGTGTACTAAAAGATGTTAA 138
           |||||||| |||  ||  ||||||
Db     279 TGCTGGTGCACTCGAAACTGTTAA 302


RESULT 5
BI321308
LOCUS       BI321308                366 bp    mRNA    linear   EST 29-NOV-2001
DEFINITION  saf50c11.y3 Gm-c1077 Glycine max cDNA clone GENOME SYSTEMS CLONE
            ID: Gm-c1077-2037 5' similar to SW:10KD_VIGUN P18646 10 KD PROTEIN
            PRECURSOR ;, mRNA sequence.
ACCESSION   BI321308
VERSION     BI321308.1  GI:15000494
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 366)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 343.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1077-2037"
                     /clone_lib="Gm-c1077"
                     /tissue_type="18 day old 'Williams' seedlings"
                     /dev_stage="18 day old 'Williams' seedlings"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The mRNA was isolated from cotyledons of 18-day-old
                     'Williams' seedlings which were greenhouse grown in
```

potting soil. The cotyledons were flash- frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/ul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately 1ml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."

BASE COUNT 124 a 60 c 70 g 112 t
ORIGIN

Query Match 35.5%; Score 49; DB 13; Length 366;
Best Local Similarity 71.9%; Pred. No. 8.7e-06;
Matches 64; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
Qy      50 GTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACT 109
           | || ||   ||||||||  | ||||||| ||    | || || || || |||||||| |
Db       3 GCTGCGATGATCACTGCAAGAACAAAGAGCACTTGCTCAGAGGCAGATGCAGGGACGATT 62

Qy     110 TCCGCTGCTGGTGTACTAAAAGATGTTAA 138
           | ||||| ||||| || ||||  ||||||
Db      63 TTCGCTGTTGGTGCACCAAAAACTGTTAA 91
```

RESULT 6
BQ151477
LOCUS BQ151477 574 bp mRNA linear EST 24-APR-2002
DEFINITION NF088A06LF1F1038 Developing leaf Medicago truncatula cDNA clone NF088A06LF 5', mRNA sequence.
ACCESSION BQ151477
VERSION BQ151477.1 GI:20288536
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 574)
AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
JOURNAL Unpublished (2000)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 574 Std Error: 0.00
Plate: 088 row: A column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers
source 1. .574
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF088A06LF"
/clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very young, developing, mature and senescing leaves."
BASE COUNT 198 a 104 c 104 g 167 t 1 others
ORIGIN

Query Match 31.6%; Score 43.6; DB 14; Length 574;
Best Local Similarity 66.7%; Pred. No. 0.00068;
Matches 96; Conservative 0; Mismatches 39; Indels 9; Gaps 2;

```
Qy       1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGT 54
           || ||.|||||| ||||||| |||| ||| || |||||||||||| |      || | |||
Db     140 AGGACTTGTGAGCATTTGGCTGATACATACAGAGGACCATGCTTCACGGAAGGTAGCTGT 199

Qy      55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
           ||    ||||||| | ||||| || | ||||||| | |||     |  |||| |
Db     200 GATGACCACTGCAAGAACAAAGCACACTTAATTAGTGGCACGTGCC---ATAACTTTCAA 256

Qy     115 TGCTGGTGTACTAAAAGATGTTAA 138
           || |  || ||| |||  ||||||
Db     257 TGTTTCTGCACTCAAAACTGTTAA 280
```

RESULT 7
BF633403
LOCUS BF633403 503 bp mRNA linear EST 19-DEC-2000
DEFINITION NF047E03DT1F1022 Drought Medicago truncatula cDNA clone NF047E03DT 5', mRNA sequence.
ACCESSION BF633403
VERSION BF633403.1 GI:11897561
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 503)
AUTHORS Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
JOURNAL Unpublished (2000)
COMMENT Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 503 Std Error: 0.00
Plate: 047 row: E column: 03
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers
source 1. .503
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF047E03DT"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints. "
BASE COUNT 181 a 82 c 93 g 147 t
ORIGIN

```
  Query Match             29.6%;  Score 40.8;  DB 12;  Length 503;
  Best Local Similarity   65.3%;  Pred. No. 0.0056;
  Matches   94;  Conservative    0;  Mismatches   42;  Indels    8;  Gaps    2;

Qy      1 AGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTA------GTGGTTGT 54
          || || |||||| ||||||| |||| ||| || ||||||||||| |      || | |||
Db    146 AGGACTTGTGAGCATTTGGCTGATACATACAGAGGACCATGCTTCACGGAAGGTAGCTGT 205

Qy     55 GACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGC 114
          ||    |||||||  | |||||   ||  | ||||||| |      |  |  |||| |
Db    206 GATGACCACTGCAAGAACAAAGCACACTTAATTAGTGGCACCGT--GCCATAACTTTCAA 263

Qy    115 TGCTGGTGTACTAAAAGATGTTAA 138
          || |  || ||| |||  ||||||
Db    264 TGTTTCTGCACTCAAAACTGTTAA 287


RESULT 8
BI642738
LOCUS       BI642738                438 bp    mRNA    linear   EST 10-SEP-2001
DEFINITION  TZS1161 TZS (Sapwood-heartwood transition zone of black locust -
            Summer) Robinia pseudoacacia cDNA, mRNA sequence.
ACCESSION   BI642738
VERSION     BI642738.1  GI:15544948
KEYWORDS    EST.
SOURCE      Robinia pseudoacacia.
  ORGANISM  Robinia pseudoacacia
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae;
            Robinia.
REFERENCE   1  (bases 1 to 438)
  AUTHORS   Han,K.-H., Yang,J., Park,S., Paule,C.R., Kapur,V., Retzel,E.F.,
            Kamdem,D.P. and Keathley,D.E.
  TITLE     Analysis of gene expression patterns in trunk wood of a mature
            black locust (Robinia pseudoacacia)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kyung-Hwan Han
            Department of Forestry
            Michigan State University
            126 Natural Resources, East Lansing, MI 48824-1222, USA
            Tel: 517 353 4751
            Fax: 517 432 1143
            Email: hanky@msu.edu.
FEATURES             Location/Qualifiers
     source          1. .438
                     /organism="Robinia pseudoacacia"
                     /db_xref="taxon:35938"
                     /clone_lib="TZS (Sapwood-heartwood transition zone of
                     black locust - Summer)"
                     /tissue_type="sapwood-heartwood transition zone"
                     /dev_stage="mature tree"
                     /note="Vector: lambda TriplEx; Site_1: Sfi IA; Site_2: Sfi
                     IB; The cDNA library was made from the sapwood-heartwood
                     transition zone of a mature black locust tree collected in
                     Michigan in late July."
BASE COUNT      134 a     80 c     86 g    124 t     14 others
ORIGIN

  Query Match             28.0%;  Score 38.6;  DB 13;  Length 438;
  Best Local Similarity   63.1%;  Pred. No. 0.029;
  Matches   89;  Conservative    0;  Mismatches   45;  Indels    7;  Gaps    2;

Qy      4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATG------CTTTAGTGGTTGTGAC 57
          || ||||||||  |||| | || ||  ||||| | |||      || |  |   || |||
Db    126 ACTTGTGAGAACCTGGCTGCTACATTCAGGGGTCTATGCATCACCTCTGCTACCTGCGAC 185

Qy     58 ACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGC 117
            ||||||||    |    |  ||  | | ||||| ||||| || |||||  | ||||
Db    186 GATCACTGCAAGNTCNNNNA-CACTTACTCAGTGGCAGGTGCAGAGACGATGTTCGCTNG 244

Qy    118 TGGTGTACTAAAAGATGTTAA 138
          |||| |-| ||||  ||||||
Db    245 GGGTGCACCAAAAACTGTTAA 265


RESULT 9
AG181132/c
LOCUS       AG181132                686 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-053O17.TJ, genomic survey
            sequence.
ACCESSION   AG181132
VERSION     AG181132.1  GI:16710812
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
            Male BAC Library clone:RP43-053O17.TJ.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 686)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .686
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-053O17.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      179 a    147 c    160 g    200 t
ORIGIN

  Query Match             25.5%;  Score 35.2;  DB 17;  Length 686;
  Best Local Similarity   55.8%;  Pred. No. 0.48;
  Matches   67;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy      8 GTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCA 67
          | |  |||  ||| || |  ||| |||   ||| ||   | |||| || || ||   |
Db    531 GGGTAAATGAGGCTGAGACCTATTGGGCTGCATTCTCAGGAGGTTATGGCATTCTAAGTC 472

Qy     68 CAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACTA 127
          |  | | |  | |  ||| ||| ||||| ||||    |    |  ||||| | || ||
Db    471 ACAGGATAAAACAGGAGGTTGGTGTAAGGTATAGGTCACAAAGACCTTGCTGATATAATA 412


RESULT 10
BG247486/c
LOCUS       BG247486                1637 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602360241F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4488491 5',
            mRNA sequence.
ACCESSION   BG247486
VERSION     BG247486.1  GI:12757301
KEYWORDS    EST.
SOURCE      house mouse.
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```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1637)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10335  row: b  column: 12
            High quality sequence start: 48
            High quality sequence stop: 200.
FEATURES             Location/Qualifiers
     source          1. .1637
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4488491"
                     /clone_lib="NCI_CGAP_Mam1"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="10 months, virgin"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT      413 a    397 c    448 g    378 t      1 others
ORIGIN

  Query Match             23.6%;  Score 32.6;  DB 12;  Length 1637;
  Best Local Similarity   55.9%;  Pred. No. 5.2;
  Matches   62;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy      16 TTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAA 75
           | ||||     | |  | |   ||||   | |  | ||||||  ||||| ||| ||||
Db     376 TGGGCATCCCGAGACTGCGCGACATGACATGGACGATGTGACTGTCACTACACGACCAGT 317

Qy      76 GAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGTACT 126
           |    ||| |   ||  | |  ||||||  | |  ||||||  | ||| |
Db     316 CATGTGGCACTGTCTGTGAAGCATAGGGAGCAATAGCGCTGCACGAGTAAT 266


RESULT 11
AQ793341/c
LOCUS       AQ793341                542 bp    DNA     linear   GSS 03-AUG-1999
DEFINITION  HS_5439_A1_F02_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=1015 Col=3 Row=K, DNA sequence.
ACCESSION   AQ793341
VERSION     AQ793341.1  GI:5700965
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 542)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 1015  row: K  column: 3
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 542.
FEATURES             Location/Qualifiers
     source          1. .542
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=1015 Col=3 Row=K"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /sex="male"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
BASE COUNT      169 a    116 c     99 g    155 t      3 others
ORIGIN

  Query Match             23.0%;  Score 31.8;  DB 17;  Length 542;
  Best Local Similarity   59.3%;  Pred. No. 6.1;
  Matches   54;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy      43 TTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGG 102
           ||| ||| | | | |  ||| | ||||   || |  | | |  ||  |  ||||  |||
Db     367 TTTGGTGCTAGCGCCTGTCAGTTCACAGGTAAGGGCACCACCATTCATAAAAGGCTTAGT 308

Qy     103 GACGACTTCCGCTGCTGGTGTACTAAAAGAT 133
           || |||||   |  |||| |  |||||| |
Db     307 AACTACTTCTAATTTTGGTTTGGTAAAAGTT 277


RESULT 12
AZ512910/c
LOCUS       AZ512910                433 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0358I17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0358I17 R, DNA sequence.
ACCESSION   AZ512910
VERSION     AZ512910.1  GI:10694226
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0358  row: I  column: 17
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
```

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          High quality sequence stop: 433.
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0358I17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      109 a    105 c     81 g    138 t
ORIGIN

  Query Match             22.5%;  Score 31;  DB 17;  Length 433;
  Best Local Similarity   51.9%;  Pred. No. 10;
  Matches   70;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy       4 ACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCAC 63
           | | || |   || |  | |||   |        |||  ||  | ||  ||  || ||  |
Db     293 AAAGGTCACCCTTAGCTACATAGCGAGTTTAAGCCAGCCTAGAATGCCTGGCACCCTGTC 234

Qy      64 TGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGACGACTTCCGCTGCTGGTGT 123
           || | ||  ||| |||  |  ||    |||  |  |||| || || |  |||  |
Db     233 TGAAAAAAAAAAAAGAGGGGGGTGGTAGGAGTGGCTAGGAACTACCTTAGCTAGTAACTG 174

Qy     124 ACTAAAAGATGTTAA 138
            || ||||  |||||
Db     173 GCTTAAAGTGGTTAA 159


RESULT 13
BE330295
LOCUS       BE330295                567 bp    mRNA    linear   EST 04-DEC-2001
DEFINITION  so75h05.y1 Gm-c1040 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1040-1522 5' similar to TR:Q9ZVJ0 Q9ZVJ0 T6A23.12 PROTEIN. ;,
            mRNA sequence.
ACCESSION   BE330295
VERSION     BE330295.1  GI:9204071
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 567)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Huntsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            Insert Length: 1479   Std Error: 0.00
            High quality sequence stop: 468.
FEATURES             Location/Qualifiers
     source          1. .567
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1040-1522"
                     /clone_lib="Gm-c1040"
                     /tissue_type="Hypocotyl and Plumule, germinating seeds"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3Pac (Pharmacia); Site_1: EcoRI;
                     Site_2: NotI; This cDNA library was constructed from mRNA
                     isolated from hypocotyl and plumule tissues of seeds
                     germinated for three days of the cultivar Williams 82.
                     Complementary DNA was synthesized from mRNA using a primer
                     consisting  of a poly(dT) sequence with a NotI restriction
                     site. EcoRI adapters were  ligated to the blunt-ended cDNA
                     fragments followed by digestions with EcoRI  and NotI. The
                     cDNA fragments were directionally cloned into the
                     EcoRI-NotI restriction site of the pT7T3-Pac vector. The
                     ligated cDNA fragments were transformed into DH10B host
                     cells (Gibco BRL). This library was constructed by Dr.
                     Randy Shoemaker."
BASE COUNT      153 a    106 c    138 g    168 t      2 others
ORIGIN

  Query Match             22.3%;  Score 30.8;  DB 10;  Length 567;
  Best Local Similarity   58.9%;  Pred. No. 13;
  Matches   53;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy       6 ATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTG 65
           |||  | ||    |||| || ||  |    ||||| | |||| | ||  | ||   | ||
Db     350 ATGCCAAAAGGCAGCAGTTATATGAATATTACCATCCATTAGAGTTTTCGCCAAATATTG 409

Qy      66 CACAACCAAAGAGAACGCAGTTAGTGGAAG 95
            ||    ||||| |||  || |  ||||||
Db     410 GACTTGAAAAGAAAACAAAGCTCATGGAAG 439


RESULT 14
BB356735/c
LOCUS       BB356735                662 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  BB356735 RIKEN full-length enriched, adult male corpus striatum Mus
            musculus cDNA clone C030017B09 3', mRNA sequence.
ACCESSION   BB356735
VERSION     BB356735.2  GI:16405759
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 662)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     On Jul 12, 2000 this sequence version replaced gi:9068563.
            Contact: Yoshihide Hayashizaki
```

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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Location/Qualifiers
source 1. .662
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C030017B09"
/clone_lib="RIKEN full-length enriched, adult male corpus striatum"
/sex="male"
/tissue_type="corpus striatum"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT 142 a 193 c 149 g 178 t
ORIGIN

Query Match 22.3%; Score 30.8; DB 10; Length 662;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 56; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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Qy       7 TGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGTGGTTGTGACACTCACTGC 66
           || | | |   || |||||| |  || |  ||  ||  ||   |||| | | | |
Db     464 TGCGGGGAGGGGGGAGATAAAAACGGGTGGGCAAACTGCAGCACTTGTTAAATTAAAGAA 405

Qy      67 ACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAGGGA 104
           |||| | || || ||| |    | ||| || |  ||||
Db     404 ACAAACTAAAAGCACGAAAAATGGGGATGGGGAGGGGA 367
```

RESULT 15
AZ395343
LOCUS AZ395343 149 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0159O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0159O08 F, DNA sequence.
ACCESSION AZ395343
VERSION AZ395343.1 GI:10510331
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 149)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0159 row: O column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 149.

FEATURES Location/Qualifiers
source 1. .149
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0159O08"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 48 a 23 c 35 g 43 t
ORIGIN

Query Match 22.2%; Score 30.6; DB 17; Length 149;
Best Local Similarity 68.9%; Pred. No. 8.9;
Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy      40 TGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGT 99
           | ||| |  | ||||||||  ||  ||  || ||| ||||| | ||  | |||||||||
Db      21 TCCTTAACAGTTTGTGACATGCATGGCTAAAGCAATGAGAAAGAAGAAAATGGAAGGTGC 80

Qy     100 A 100
           |
Db      81 A 81
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Job time : 505.799 secs

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